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## OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 74.81 Seconds  
(Without alignments)  
3473.870 Million cell updates/sec

Title: US-09-852-845-1  
Perfect score: 1058  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

## Database :

Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/1/lna/5B.COMB.seq:\*  
3: /cgn2\_6/ptodata/1/lna/6A.COMB.seq:\*  
4: /cgn2\_6/ptodata/1/lna/6B.COMB.seq:\*  
5: /cgn2\_6/ptodata/1/lna/PCTUS.COMB.seq:\*  
6: /cgn2\_6/ptodata/1/lna/backfiles1.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	814.4	77.0	848	1	US-08-192-480A-1
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C 40	42.4	4.0	1724	5	PCT-US96-12374-1	Sequence 1, Appl
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C 42	42	4.0	3923	3	US-08-860-635A-20	Sequence 20, Appl
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C 45	41.6	3.9	30001	1	US-08-125-468-1	Sequence 1, Appl

## ALIGNMENTS

RESULT 1  
US-08-147-784-1  
Sequence 1, Application US/08147784  
Patent No. 5821332  
GENERAL INFORMATION:  
APPLICANT: Godfrey, Wayne  
APPLICANT: Buck, David  
APPLICANT: Engleman, Edgar G.  
TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
TITLE OF INVENTION: CD4+ T-CELLS: ACT-4  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESS: Townsend and Townsend Kourie and Crew  
STREET: 379 Lytton Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: US  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/147,784  
FILING DATE: 03-NOV-1993  
CLASSIFICATION: 424  
ATTORNEY/AGENT INFORMATION:  
NAME: Smith, William M.  
REGISTRATION NUMBER: 30,223  
REFERENCE/DOCKET NUMBER: 05490A-220  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 326-2400  
TELEFAX: (415) 326-2422  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1057 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 15..845  
OTHER INFORMATION: /standard\_name="ACT-4 cDNA"  
US-08-147-784-1  
Query Match 98.7%; Score 1044.4; DB 1; Length 1057;

Best Local Similarity 99.8%; Pred. No. 3.2e-189;  
Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

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; Patent No. 6242566
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/195,967
; FILING DATE: 10-FEB-1994
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 05490A-230
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 326-2400
; TELEFAX: (415) 326-2422
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1057 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHEICAL: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..845
; OTHER INFORMATION: /standard_name="ACT-4 cDNA"
US-08-195-967-1

Query Match 98.7%; Score 1044.4; DB 4; Length 1057;
Best Local Similarity 99.8%; Pred. No. 3.2e-189;
Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

OY 1 cagcagaagacgaagatgctgctgagggcctcgagctgagccgagccgctgctgagcctc 60
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1 COMPUTER READABLE FORM:
2 MEDIUM TYPE: Floppy disk
3 COMPUTER: IBM PC compatible
4 OPERATING SYSTEM: PC-DOS/MS-DOS
5 SOFTWARE: Patent In Release #1.0, Version #1.25
6 CURRENT APPLICATION DATA:
7 APPLICATION NUMBER: US/08/472,940
8 FILING DATE: 06-JUN-1995
9 CLASSIFICATION: 530
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: US 08/147,784
12 FILING DATE: 03-NOV-1993
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Smith, William M
15 REGISTRATION NUMBER: 30,223
16 REFERENCE/DOCKET NUMBER: 05490A-220
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (415) 326-2400
19 TELEFAX: (415) 326-2422
20 INFORMATION FOR SEQ ID NO: 1:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 1057 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: single
25 TOPOLOGY: linear
26 MOLECULE TYPE: cDNA
27 HYPOTHETICAL: NO
28 FEATURE:
29 NAME/KEY: CDS
30 LOCATION: 15..845
31 OTHER INFORMATION: /standard_name="ACT_4 cDNA"
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; Patent No. 6277962
; GENERAL INFORMATION:
; APPLICANT: Godfrey, Wayne
; APPLICANT: Buck, David
; APPLICANT: Engleman, Edgar G.
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend Kourile and Crew
; STREET: 379 Lytton Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: US
; ZIP: 94301

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	Query Match	98.7%	Score 1044.4	DB 4	Length 1057	
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RESULT 4				
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Sequence 1, Application US/08192480A				
Patent No. 5759546				
GENERAL INFORMATION:				
APPLICANT: Andrew D. Weinberg and Arthur A.				
APPLICANT: Vandenbark				
TITLE OF INVENTION: TREATMENT OF CD4 T-CELL				
TITLE OF INVENTION: MEDIATED CONDITIONS				
NUMBER OF SEQUENCES: 3				
CORRESPONDENCE ADDRESS:				
ADDRESSEE: Richard J. Polley, Esq.				
ADDRESSEE: Klarquist Sparkman Campbell				
ADDRESSEE: Leigh A. Whinston				
STREET: 121 S.W. Salmon Street, Suite 1600				
CITY: Portland				
STATE: Oregon				
COUNTRY: United States of America				
ZIP: 97204				
COMPUTER READABLE FORM:				
MEDIUM TYPE: Disk, 3-1/2 inch				
COMPUTER: IBM PC compatible				
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FILING DATE:				
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FILING DATE:				
ATTORNEY/AGENT INFORMATION:				
NAME: Richard J. Polley, Esq.				
REGISTRATION NUMBER: 28,107				
REFERENCE/DOCKET NUMBER: 4282-38649				

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; Sequence 10, Application US/08097827

Query Match	27.1%	Score 286.6	DB 1	Length 1317
Best Local Similarity	66.6%	Pred. Nt. 3e-45		
Matches	428	Conservative	0	Mismatches 209; Indels 6; Gaps 1
OY	87	accgtgacgggagctcactatgttcggggagacctaccaccagaacgaccggtgtccac	146	
	11			
Db	61	ACAGCAAGCGGGCTCAACTGTGTAAATATACTACCCACCGATGATCACAAGTGTCTCGT	120	
	147	gaattcaggccagcgaaacggagatgtgtgacccctcagcggctcccaagaacggtgtgc	206	
	121			
Db	121	GAGTCCAGCCAGCGGCATGTGTGTGTGAACCCCTGTGATCATACCGAGGATTACTCTATGT	180	
	207	cgctccgtgcgggacgggtcttacaagaacgtgtgtcagctccaaagccgtgtgcaagccctgc	266	
	1			

Db	181	CATCCGCTGTGAGACTGGCTTTACAAATGAAGCTCTCAATTATGATTAATCTGCAAAGCAAGTGT	240
Oy	267	acgtggtgtaaaccttaagaagtgggagtgtagaggaagcagctgtgcaagcgccacaagagac	326
Db	241	ACACAGCTCAACCAATCGAAGTGAAGTGAATCTCAAGCAGAGATTCCACCTACTACAGAT	300
Oy	327	acagctctccgctcccgagcgaggagaccagagcccttgca-----cagctacaagccgtga	380
Db	301	ACTGCTCTCAATGTATGACACGAGCACCACCAACTCTGGCAGCAGCGGCTCAAGCTTGGA	360
Oy	381	gttgacgtgtgccccctgcccctccacggggcaacttctcccaaggcgagcaacccagagcctgcaag	440
Db	361	GTTGACTGTGTTCCCTCGCCCTCTGCGCACCATTTCACGAGCAACACAGGCGTGCAG	420
Oy	441	cccttgaccacactgacacttgctctggggaagagaccccttgagccggcgacgaatagtctg	500
Db	421	CCCTGGACCAATTGTACTTATCTTGGAAGACAGACCCGCCACCCAGCCAGTGAACAGTTTG	480
Oy	501	gacgaacatctgttgaggaagagagaccccccagaccagccagccgcccagagaccacagggcccc	560
Db	481	GACGCAGCTGTGAGAGACAGAAGCGTCTCTGGCCACACTGCTCTGTGGAGACCCAGCGCCT	540
Oy	561	ccggagccagagcccaatcaactgttccagcccaactgaaagcctctggccccagaaacctcaagggacc	620
Db	541	ACATTCAAGGCCAACCACTGTCCAAATCCACACCACTATCTGGCCACAGACTTGTGAGTTGCC	600
Oy	621	tccacccggagccgttgagagtcctccgggggacggttgagttgcccgcacatccttggagccttgg	680
Db	601	TCTACACCCACCTTGGTGTGAGACCCAGATCTGTGTACAAAACTCAACATGCCCAACGCTGC	660
Oy	681	ctgtgtgtctggggctgtgtgtggccccccttgagccatcctctgtctgccc	723
Db	661	CCAGCACCTTGAAGCCGAGGGGGGCCCGCTCACTTCTTCCTTCC	703

RESULT 6  
US-08-494-574-10  
; Sequence 10, Application US/08494574  
; Patent No. 5783665  
; GENERAL INFORMATION:  
; APPLICANT: Baum, Peter  
; APPLICANT: Goodwin, Ray  
; APPLICANT: Fanslow, William  
; APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for  
TITLE OF INVENTION: OX40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,574  
FILING DATE: 22-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:  
LENGTH: 1317 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOX40Fc Muteln  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1317  
US-08-494-574-10

Query Match 27.1%; Score 286.6; DB 1; Length 1317;  
Best Local Similarity 66.6%; Pred. No. 36-46;  
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

QY 87 accgtgacgggctccactgtgtcgaggacacctaccacagacgaccggtgtgtcac 146  
DB 61 ACAGCAAGGCGGCTCAACGTGTAAACATACCTACCCAGTGTCTCAGTGTCTGCT 120  
QY 147 gaggtagcaggcagggcagcagcagcagcagcagcagcagcagcagcagcagcag 206  
DB 121 GAGTGCACACCCAGGCGCATGTGTGTGACACCGCTGTGATCATACCGGATACCTATGT 180  
QY 207 cgtccgtgagcggcggcggcgttctacacagcgtgtgtcagcagcgtgtgtgtgtc 266  
DB 181 CATCGGTGTGAGACGTGTCTTACATGAACTGTCAATTATGATACCTGTCAAGCAGTGT 240  
QY 267 acgtgtgtgtacacctcagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 326  
DB 241 ACACAGTGAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300  
QY 327 acaagtcgcgcgtccgcggcggcggcggcggcggcggcggcggcggcggcggcggc 380  
DB 301 ACTGTGTGAGATGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 360  
QY 381 gttagactgtgccccctgccccctcagggcactctctccagggcagacacagggcgtga 440  
DB 361 GTTGAAGTGTGTCCCTGCGCCCTGCGCCACTTTTTCAGGCAACACAGCGCTGTCAAG 420  
QY 441 cccttgaccacactgtcaccttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 500  
DB 421 CCTGTGACCAATTGTACTTATCTGTGAAGACAGACCCGCGCACCCAGCTGACACTTG 480  
QY 501 gacgcaatctgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 560  
DB 481 GACGCACTGTGTGAGACAGAAAGCCTCTGCGCACACTGTCTGTGGAGACACCGCCCT 540  
QY 561 ccggcagcagccacatcactgtlccagcccaactgaagcctgtgcagcagaaacctcaagggacc 620  
DB 541 ACATTTCAGGCGCAACCACTCTCCATCCACACAGCTGTGGCCCGAGGACTCTGTGAGTTGCC 600  
QY 621 tccacccggcggcgt 680  
DB 601 TCTACACCCACCTTGTGTGAAGCCCAAGATTGTGTGACAAATCTACACATGCCCCACGCTGC 660  
QY 681 cgt 723  
DB 661 CCAGCACTGTGAAGCCGAGGCGCGCGCTGTCTCTCTCTCTCTCTCTCTCTCTCTCT 703

RESULT 7  
US-08-097-827-6  
Sequence 6, Application US/08097827  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
Goodwin, Ray  
Fanslow, William  
Gayle, Richard

TITLE OF INVENTION: Novel Cytokine which is a ligand for  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-Jul-1993  
CLASSIFICATION: <unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOUSE OX40  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..618  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-097-827-6

Query Match 26.8%; Score 283.2; DB 1; Length 618;  
Best Local Similarity 70.6%; Pred. No. 136-45;  
Matches 394; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

QY 87 accgtgacgggctccactgtgtcgaggacacctaccacagacgaccggtgtgtcac 146  
DB 61 ACAGCAAGGCGGCTCAACGTGTAAACATACCTACCCAGTGTCTCAGTGTCTGCTGTGT 120  
QY 147 gaggtagcaggcagggcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 206  
DB 121 GAGTGCACACCCAGGCGCATGTGTGTGACACCGCTGTGATCATACCGGATACCTATGT 180  
QY 207 cgtccgtgagcggcggcgttctacacagcgtgtgtcagcagcagcagcagcagcagcagc 266  
DB 181 CATCGGTGTGAGACGTGTCTTACATGAACTGTCAATTATGATACCTGTCAAGCAGTGT 240  
QY 267 acgtgtgtgtacacctcagaaagtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 326  
DB 241 ACACAGTGAACAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 300  
QY 327 acaagtcgcgcgtccgcggcggcggcggcggcggcggcggcggcggcggcggcggc 380  
DB 301 ACTGTGTGAGATGTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGC 360  
QY 381 gttagactgtgccccctgccccctcagggcactctctccagggcagacacagggcgtga 440  
DB 361 GTTGAAGTGTGTCCCTGCGCCCTGCGCCACTTTTTCAGGCAACACAGCGCTGTCAAG 420  
QY 441 cccttgaccacactgtcaccttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 500

best local similarity 70.08; fixed, no. 1.06 42;  
Matches 394; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

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; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/027

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RESULT 9  
 US-08-911-423-3  
 : Sequence 3, Application US/08911423  
 : Patent No. 6111090  
 :  
 : GENERAL INFORMATION:  
 :  
 : APPLICANT: Gorman, Daniel M.  
 : APPLICANT: Randall, Troy D.  
 : APPLICANT: Zlotnick, Albert  
 : TITLE OF INVENTION: MAMMALIAN CELL SURFACE ANTIGENS; RELATED  
 : TITLE OF INVENTION: REAGENTS  
 : NUMBER OF SEQUENCES: 8  
 :  
 : CORRESPONDENCE ADDRESS:  
 :  
 : ADDRESSEE: DNAX Research Institute  
 : STREET: 901 California Avenue  
 : CITY: Palo Alto  
 : STATE: California  
 :  
 : COUNTRY: USA  
 : ZIP: 94304-1104  
 :  
 : COMPUTER READABLE FORM:  
 : MEDIUM TYPE: Floppy disk  
 : COMPUTER: IBM PC compatible  
 : OPERATING SYSTEM: PC-DOS/MS-DOS  
 : SOFTWARE: PatentIn Release #1.0, Version #1.30  
 :  
 : CURRENT APPLICATION DATA:  
 : APPLICATION NUMBER: US/08/911,423  
 : FILING DATE: 14-AUG-1997  
 : CLASSIFICATION: 536  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/023,419  
 : FILING DATE: 16-AUG-1996  
 : PRIOR APPLICATION DATA:  
 : APPLICATION NUMBER: US 60/027,901





```

RESULT 13
US-08-259-924-1
: Sequence 1, Application US/08259924
: Patent No. 5563064
: GENERAL INFORMATION:
: APPLICANT: HUTCHINSON, Charles R.
: APPLICANT: MADUDURI, Krishna M.
: APPLICANT: TORRI, Francesca
: APPLICANT: COLOMBO, Anna L.
: TITLE OF INVENTION: PROCESS FOR PREPARING DAUNORUBICIN
: NUMBER OF SEQUENCES: 6
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Nikolaide, Marmelstein, Murray & Oram
: STREET: 655 Fifteenth Street N.W. Suite 330
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.
: ZIP: 20005-5701
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentln Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/259,924
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 793,873
: FILING DATE: 18-NOV-1991
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/959,941
: FILING DATE: 09-OCT-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Kilts, Monica C.
: REGISTRATION NUMBER: 36,105
: REFERENCE/DOCKET NUMBER: 1615-4003
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202)638-5000
: TELEFAX: (202)638-4810
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1632 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 204..1271
US-08-259-924-1

Query Match 4.6%; Score 48.2; DB 1; Length 1632;
Best Local Similarity 48.8%; Pred. No. 0.29;
Matches 187; Conservative 0; Mismatches 193; Indels 3; Gaps 2.

655 cagttgcgcagcctctggggccctgggcccgtgctgggggccccctggcgcaccc 714
Db 220 CGGTGCGGCGCCCGGCGGCGACGATCGAGCGCCCTGAGGACCTGTATCCGCTGGAGGCG 279

715 tgcctggccctgtacctgtctcggagagagacagaggctgcgcccccgatggccacaagcccc 774
Db 280 TGCACAGCCGCCATGCTGCTGCGAGAGGCGCCGACCCCTGGGGCTCTGACACATCTCTGG 339

775 ctgggggagagcaagttccggagccc--ccatccaaagagagcagggccagagcccaactccac 832
Db 340 CCGGGGCGCCGACACCTGTGAAGGCCCTTGGCGGGCCAGAGACAGACACCCGGCGGAAGCACTCC 399

833 cctggccaagatcctgaccttggggcccaacaagaagtgtgaagcttg--ggcccccgaaggtctga 891
Db 400 TCGCGCTGATCCGCGCACCTGGTGCGATTCGACTGCTCGAGGAGGACGACCCGGGCGACT 459

```

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QY      892 gcccgaggggtctgctggcgcggagggaagtgtgaagcgccctccccccaagctctt 951
Db      460 TGTGTCGCCGACCGAGGCTGGCAGACTGCTCCGCAGCACCAACCAGCCGCGACGGTCT 519
QY      952 gggcaactctgcacgcttcctagtgatgcgatgtgctgcctcgcgtctctgattacgtatg 1011
Db      520 GGCACGACTGTACGACGAGGCGTGGGCGCGCCGACATCTCTTCAACCCGCGTCCCGAAG 579
QY      1012 ccatacatcctctgcgccgcgcg 1034
Db      580 CCATCGTAGCCGCGCCCCACG 602

RESULT 14
US-08-794-796-1
; Sequence 1, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; PRIOR APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO.: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1164 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-794-796-1

Query Match          4.5%; Pred. 47.2; DB 2; Length 1164;
Best Local Similarity 46.4%; Pred. No. 0.43;
Matches 154; Conservative 0; Mismatches 178; Indels 0; Gaps 0.

QY      19 gcgttgaggagctggcgagctgggcgcgcgggcccgttgtgcgagctctgctcctcctgggacctgg 78
Db      133 GCCTGTGCGTGCTGTGGCTGGTGTTGGGGCGTGCCTGCCCCTGCTGCGCGGAGCCGGCGTATC 192
QY      79 gacttgagcacgctgacgggggtcccaactgtgtctcggggacaacctaacccagaacgacggt 138

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Db 193 GCGAGTGGCAGAAACACCCCTACCCCTGGGGACGACAGACAGGGGAGCGGCTGG 252  
QY 139 gctgcacagagtgacagcgaagcgaagatggtgagccgtgcagccgtccccaaga 198  
Db 253 TGTGGCCCGCAGTGGCCCCCAGGACCTTGTGTGACAGCGGCGGTGCCGCGAGACAGCCCA 312  
QY 199 cgtgtgcgtcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 258  
Db 313 CGAGGTGTGGCCGCTGTCCACCGCGCTACACGCACTGTGAACTACTGTGAGCGCT 372  
QY 259 agccctgacgtgtgttaacctcagaagtgtgagtgagcgaagcgtgtgcagcgca 318  
Db 373 GCCGCTACTGCAACGCTCTGTGGGGGAGCGGTGAGAGAGGACAGGGGCTTGCCAGGCCA 432  
QY 319 cacaagacacagctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 350  
Db 433 CCCACAAACCGTGGCTGCGCGCTGCGCACCGGC 464

RESULT 15  
US-09-286-529-18  
; Sequence 18, Application US/09286529  
; Patent No. 6297367  
; GENERAL INFORMATION:  
; APPLICANT: Catherine Tribouley  
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES  
; FILE REFERENCE: 1408.003/200130.439C1  
; CURRENT APPLICATION NUMBER: US/09/286,529  
; CURRENT FILING DATE: 1999-04-05  
; NUMBER OF SEQ ID NOS: 25  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 18  
; LENGTH: 1347  
; TYPE: DNA  
; ORGANISM: Homo sapien  
US-09-286-529-18

Query Match 4.5%; Score 47.2; DB 4; Length 1347;  
Best Local Similarity 46.4%; Pred. No. 0.44;  
Matches 154; Conservative 0; Mismatches 178; Indels 0; Gaps 0;  
QY 19 gctgtgggggctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 78  
Db 340 gctgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 399  
QY 79 gcttgagcaccgtgcagggggtcctcactgtgtcggggacacctaccacgaacgacggt 138  
Db 400 gctgagatggcagaacacaccacctacccttgccgagcagagagggagcggtg 459  
QY 139 gctgcacagagtgacagcgaagcgaagatggtgagccgtgcagccgtccccaaga 198  
Db 460 tgtgcgccagtgccccccagacacttgtgcagcggcgtgcgtgcgtgcgtgcgtgc 519  
QY 199 cgtgtgcgtcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 258  
Db 520 cgaactgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 579  
QY 259 agccctgacgtgtgttaacctcagaagtgtgagtgagcgaagcgtgtgcagcgca 318  
Db 580 gctgactatgcaacgtctctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 639  
QY 319 cacaagacacagctgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 350  
Db 640 ccaacacacgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgcgtgc 671

Search completed: June 18, 2002, 17:24:04  
Job time: 10162 sec



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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: June 18, 2002, 14:23:57 ; Search time 17.68 Seconds  
(without alignments)  
1505.472 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 1538

Sequence: 1 MCVGARRLRGRCPCALLLLG.....SFRTPRQEOADAHSTLAKI 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283138 segs, 96089334 residues

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1538	100.0	277	2	137552
2	864.5	56.2	271	2	S12783
3	857	55.7	272	2	I48700
4	224.5	14.6	427	1	GOHUN
5	221.5	14.4	277	2	A60771
6	217	14.1	461	1	A35356
7	216	14.0	425	1	A26431
8	211.5	13.8	416	1	JN0006
9	209.5	13.6	435	2	I54182
10	209	13.6	305	2	A46476
11	202.5	13.2	256	2	B32393
12	202.5	13.2	474	2	B38634
13	201.5	13.1	459	2	I48854
14	186.5	12.1	255	2	I38426
15	172	11.2	461	1	GOH71
16	171	11.1	327	2	A46484
17	168.5	11.0	651	2	JC7705
18	161	10.5	454	1	GOMST1
19	160.5	10.4	325	2	B43692
20	152	9.9	326	1	GOVZML
21	149.5	9.7	260	1	A46517
22	147.5	9.6	324	1	JC2395
23	147	9.6	595	2	A42086
24	146.5	9.5	348	2	T28623
25	146.5	9.5	349	2	D36858
26	145.5	9.5	349	2	D72175
27	144	9.4	461	1	JC4302
28	142	9.2	250	1	A49033
29	139	9.0	3075	2	S14458

30	138	9.0	1798	2	S53869	laminin beta-2 cha
31	132	8.6	1801	1	MMRTS	laminin beta-2 cha
32	128.5	8.4	1713	2	A55347	adhesive ligand ep
33	128	8.3	3635	2	T10053	laminin alpha 5 ch
34	127.5	8.3	3707	2	S18252	heparan sulfate pr
35	127	8.3	1808	2	T15099	hypothetical prote
36	126.5	8.2	3106	1	S53868	laminin alpha-2 cha
37	126	8.2	1797	2	A55677	laminin beta-2 cha
38	126	8.2	4391	2	A38096	pelican precursor
39	125.5	8.2	722	2	I48324	DELTA-like 1 - mou
40	125	8.1	1557	2	T28811	hypothetical prote
41	124.5	8.1	455	1	GOH71	tumor necrosis fac
42	122.5	8.0	1111	2	T26972	hypothetical prote
43	122.5	8.0	1254	2	I48161	p-185 precursor -
44	122	7.9	3672	2	T23433	hypothetical prote
45	122	7.9	3704	2	T37316	probable laminin a

#### ALIGNMENTS

RESULT 1  
137552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnitger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CA53576.1; PID:9472958  
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 100.0%; Score 1538; DB 2; Length 277;  
Best local Similarity 100.0%; Pred. No. 5e-94;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY	1	MCVGARRLRGRCPCALLLLGLSTVGTGHCVDTPPSNDRCHCRPGNGVSCRSQ	60
DB	1	MCVGARRLRGRCPCALLLLGLSTVGTGHCVDTPPSNDRCHCRPGNGVSCRSQ	60
OY	61	NTVCAPCGPGFYNDVSSKPKCKTWCNLRSGSERKOLCTATQDTPVCRAGTOPLDSYK	120
DB	61	NTVCAPCGPGFYNDVSSKPKCKTWCNLRSGSERKOLCTATQDTPVCRAGTOPLDSYK	120
OY	121	PCVDCAPCPGPHFSPGDNACKPWTNCTLAGHTTQPSNSSDAICEDRDPATPOETQ	180
DB	121	PCVDCAPCPGPHFSPGDNACKPWTNCTLAGHTTQPSNSSDAICEDRDPATPOETQ	180
OY	181	GPPAPRTVQPTPEAMPRTSQGSPTRVEVPGGRAVAALIGLVLGLPLAIIATLYL	240
DB	181	GPPAPRTVQPTPEAMPRTSQGSPTRVEVPGGRAVAALIGLVLGLPLAIIATLYL	240
OY	241	RRDQRLPPDAHKKPCGSGSFRTPRQEOADAHSTLAKI	277
DB	241	RRDQRLPPDAHKKPCGSGSFRTPRQEOADAHSTLAKI	277

RESULT 2  
S12783  
OX40 antigen precursor - rat  
N:Alternate names: nerve growth factor receptor homolog  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 05-Nov-1999  
C:Accession: S12783; S08036  
R:Maliet, S.; Fossum, S.; Barclay, A.N.  
EMBO J. 9, 1063-1068, 1990



F:29-427/Product: nerve growth factor receptor #status experimental <MAT>  
 F:29-250/Domain: extracellular #status predicted <EXT>  
 F:32-65/Domain: NGF receptor repeat homology <NG1>  
 F:67-108/Domain: NGF receptor repeat homology <NG2>  
 F:109-147/Domain: NGF receptor repeat homology <NG3>  
 F:149-189/Domain: NGF receptor repeat homology <NG4>  
 F:197-248/Region: serine/threonine-rich  
 F:251-272/Domain: transmembrane #status predicted <TRM>  
 F:273-427/Domain: intracellular #status predicted <INT>  
 F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 14.6%; Score 224.5; DB 1; Length 427;  
 Best Local Similarity 30.1%; Pred. No. 8.4e-08;

Matches 84; Conservative 31; Mismatches 95; Indels 69; Gaps 16;

QY 3 VGARRLR---CP-CAALLLLGLG-----STVGLHCVGTYSNDRCHECRGNAMV 53  
 DB 1 MGAAATGAMDGPRLLLLLLGLVSLGAKKACPTGL-----YTHSGCCACMLGEGVA 54  
 QY 54 SRCRSQNTVCPCPGPF-YNDVVS-SKPCPCCTWC-NLRSGSERKQLCTADTVCR-- 108  
 DB 55 QPCGANO-TVCEPCLDSTFSDVVSATPECKPCTECVGLQSMAP---CVLADAVCRCA 110  
 QY 109 -----CRAGTQPLDSY--KGVDCAPCPHPSPGDNOA--CKPWTNC 147  
 DB 111 YGYODETTTGRCACRCVCEAGSLVFSCQDKQNTVCECCPGDTYSDEANHVDPCLPTVC 170  
 QY 148 TLAKKHTLQPAKNSSDAICED-----RDPPATQPOFTGQPPARPITVQTE 193  
 DB 171 E-DTEROLRECTRWADACEIPGRMTTRSTPPREGSDSTASTOEPAPRODL-IASTV 228  
 QY 194 AMPRTSGPSTPYE-----VPGGRAVAAILGLGLV 224  
 DB 229 AGVYTVWGSSQPVYTRGTNTNLIPVYSILAAVVGVL 267

# RESULT 5

B-cell activation protein CD40 precursor - human

N:Alternate names: B-cell surface antigen Bp50

C:Species: Homo sapiens (man)

C:Date: 03-Jun-1993 #sequence, revision 03-Feb-1994 #text, change 21-Jul-2000

C:Accession: S04460; A60771

R:Stamenkovic, I.; Clark, E.A.; Seed, B.

EMBO J. 8, 1403-1410, 1989

A:Title: A B-lymphocyte activation molecule related to the nerve growth factor receptor

A:Reference number: S04460; MUID:8935608

A:Accession: S04460

A:Molecule type: mRNA

A:Residues: 1-277 <STRA>

A:Cross-references: EMBL:X60592; NID:g29850; PIDN:CAA43045.1; PID:g29851

R:Braesch-Andersen, S.; Paulie, S.; Kono, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.

J. Immunol. 142, 562-567, 1989

A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-11k

A:Reference number: A60771; MUID:8903941

A:Accession: A60771

A:Molecule type: protein

A:Residues: 21-50 <BRA>

A:Experimental source: Burkitt lymphoma cell line Raji

C:Gene: GDB:CD40

A:Cross-references: GDB:215268; OMIM:109535

A:Map position: 20q12-20q13.2

C:Superfamily: CD27 antigen; NGF receptor repeat homology

C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane protein

F:1-20/Domain: signal sequence #status predicted <SIG>

F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>

F:194-215/Domain: extracellular #status predicted <EXT>

F:216-277/Domain: intracellular #status predicted <CYT>

Query Match 14.4%; Score 221.5; DB 2; Length 277;  
 Best Local Similarity 23.2%; Pred. No. 9.1e-08;  
 Matches 66; Conservative 34; Mismatches 95; Indels 89; Gaps 10;

QY 26 VTGLH-----CVGDTYSNDRCHECRPGNGVSRCSQNTVCPCPGPFYNDVVS 79  
 DB 15 LTAHVPEPTACREKQYLLINSQCSLCPGOKLVSDCTEFETBCLPCGESEFLDWTNRE 74  
 QY 80 P-CKPCTWCNLRSGSERKQLCTAQTQDYVCRAGTQPLD-----SVKPGVD----- 124  
 DB 75 THCHOHKYCDPNLGLRVQKGTSETDTICTCEEGHCTSEACESCVLHRSQSPGVKQI 134  
 QY 125 -----CAPCPHPSPGDN--OACKPWTNCTLAKHTLQPAKNSSDAICEDNDPPAT 174  
 DB 135 ATGVSDTICEPCPCPGPFENNSSAFCKHPWTSCEKLDLVQDAGNKTKDYVC----- 186  
 QY 175 QPQETGPPARPITYQPTPEAMPRTSGPSTPYEYVGGRAVAAILGLGLVGLLPLAIL 234  
 DB 187 -----GPQDR-----LRALVVIPIFGIL--FAIL 209  
 QY 225 LALYLRRDQRLP-----PDAKRP-----GGGSRFTPIQE 265  
 DB 210 LVLFVIRKVKARKPTNKAPRQEPQELNFPDDLPGSNTAAPVQE 253

# RESULT 6

tumor necrosis factor receptor 2 precursor [validated] - human

N:Alternate names: 75k tumor necrosis factor receptor; TNF receptor type 2

C:Species: Homo sapiens (man)

C:Date: 10-Sep-1999 #sequence, revision 10-Sep-1999 #text, change 08-Dec-2000

C:Accession: A35356; A36475; A48416; A36007; A23666; B35010; I38094

R:Smith, C.A.; Anderson, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerry, R.; Dower, Science 248, 1019-1023, 1990

A:Title: A receptor for tumor necrosis factor defines an unusual family of cellular a

A:Reference number: A35356; MUID:90260639

A:Accession: A35356

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-461 <SMT>

A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186

R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squit

Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A:Title: A second tumor necrosis factor receptor gene product can shed a naturally oc

A:Reference number: A36475; MUID:91045991

A:Accession: A36475

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-195; 'R', 197-461 <KOH>

A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA6755.1; PID:g339758

R:Dembic, Z.; Loeschner, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus,

Cytochrome 2, 231-237, 1990

A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular

A:Reference number: A48416; MUID:91370690

A:Accession: A48416

A>Status: preliminary

A:Molecule type: protein

A:Residues: 23-461 <DBM>

A:Cross-references: GB:S63368; NID:g235648; PIDN:AAI19824.1; PID:g235649

A>Note: sequence extracted from NCBI backbone (NCBI:63368, NCBI:63371)

R:Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demons

A:Reference number: A36007; MUID:90349572

A:Accession: A36007

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 116-140; 'P', 142-195; 'R', 197-362; 'T', 364-461 <HEL>

A:Cross-references: GB:M35857; NID:g339751; PIDN:AA63362.1; PID:g339752

R:Loetscher, H.; Schlaepper, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus,

J. Biol. Chem. 265, 20131-20138, 1990

A:Title: Purification and partial amino acid sequence analysis of two distinct tumor



Query Match	13.88;	Score 211.5;	DB 1;	Length 416;
Best Local Similarity	30.68;	Pred. No. 5.8e-07;		
Matches 77; Conservative	23;	Mismatches 101;	Indels 51;	Gaps 13;

```

C:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match          13.6%; Score 209.5; DB 2; Length 435;
Best Local Similarity 24.5%; Pred. No. 8.2e-07;
Matches 67; Conservative 27; Mismatches 87; Indels 93; Gaps 9;

OY 37 PSNDSCHECHPRGNOMVRCRSRSNTVCRPGCPGVNDVNVSSK-CRKCPTCNLRSGSER 95
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 53 PQRHRCRCRCPGVTVSKSKSRIRDTVCATCAENSYNEMHWYLTICQLCRCPDVMGLEE 112
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 96 KQLCATQDTVQCRAG-----TQPLDSYKPGVD-----CACP 130
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 113 IAPCTSKRKTQCRQCPGMFCAMALECTHCELLSDCPGTEBAELKDEVGKNNHCVCCKA 172
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 131 GHF--SPEDNACAKWVTCITLAKGHTLQPASNSSDAICEDRPAPATQDETQGPAPRPT 188
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 173 GHFQNTSSPSARCCPHTFCENQGLVEAAPGTAOSDPTCKN-----PLEPL- 217
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 189 VQPTAMPRTSQGPSTRVEVPGGRAVAAILGLGIYGLGLPLAILAL----- 237
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 218 -----PPMSGTM-----LMLAVLLPLAFLLLATVFSCTKSH 251
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 238 -----YLLRNDQRLPPDAHRRPGGSEFRT 262
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 252 PSLCRKLGLSLKRRPQEGPN---PVAGSNEPP 281
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

RESULT 10
A66476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2000
C:Accession: A66476; A66515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of mur
A:Reference number: A66476; MUID:92105763
A:Accession: A66476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:g1553058
A>Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBI:P:75207)
R:Grimmaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockay
J. Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A66515; MUID:93094586
A:Accession: A66515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <GR>
A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126
A:Experimental source: BALB/C, liver
A>Note: sequence extracted from NCBI backbone (NCBI:P:120357)
C:Comment: For an alternative splice form, see PIR:A66515.
C:Comment: For an alternative splice form, see PIR:A66476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match          13.6%; Score 209; DB 2; Length 305;
Best Local Similarity 22.0%; Pred. No. 6.5e-07;
Matches 64; Conservative 39; Mismatches 96; Indels 92; Gaps 9;

OY 26 VTGHH-----CVGDTPSNDRCHECHPRGGMVSRGSRSONTYCRRPGCFYNDVYSSK 79
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 15 LTAVHLGOCVTCSDKQYIHDQCCDLCPGSRILTSHCTALEKTQCHPCDSDGEFSAMQNNRE 74
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

OY 80 -PCKCTCMCNLRSGSERCOLCTATQDTVQCRAG----- 112

```







Db 246 IICRDSAP--VKVEEGEIVTKPLTPASIPAPSPNPGFNPTLGFSTTPRFSHPVSTPIS 303  
Qy 209 -----VPGGRAVAAILGLG-LVLGLGLPIAI 233  
Db 304 PVGSPSNMHNHFVPVREVPVTOGADPLLYGSLNPVPI 340

Search completed: June 18, 2002, 14:24:43  
Job time: 46 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

## OM protein - protein search, using sw model

Run on: June 18, 2002, 14:24:46 ; Search time 11.65 Seconds  
(Without alignments)  
920.628 Million cell updates/sec

Title: US-09-852-845-2  
Perfect score: 1538  
Sequence: 1 MCVGARLGRGRCALLLG.....SPRTPIQEQADAHSTLAKI 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues  
Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : SwissProt\_40:\*  
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1538	100.0	277	1	TNR4_HUMAN
2	864.5	56.2	271	1	TNR4_RAT
3	857	55.7	272	1	TNR4_MOUSE
4	248.5	16.2	415	1	TNR3_MOUSE
5	247	16.1	616	1	TR11_HUMAN
6	224.5	14.6	427	1	TR16_HUMAN
7	221.5	14.4	277	1	TNR5_HUMAN
8	221.5	14.4	625	1	TR11_MOUSE
9	217	14.1	461	1	TR1B_HUMAN
10	216	14.0	425	1	TR16_RAT
11	211.5	13.8	416	1	TR16_CHICK
12	209.5	13.6	435	1	TNR3_HUMAN
13	209	13.6	289	1	TNR5_MOUSE
14	202.5	13.2	256	1	TNR9_MOUSE
15	202.5	13.2	474	1	TR1B_MOUSE
16	194.5	12.6	283	1	TR1A_HUMAN
17	187.5	12.2	269	1	TNR5_BOVIN
18	186.5	12.1	255	1	TNR9_HUMAN
19	172	11.2	461	1	TR1A_RAT
20	171	11.1	327	1	TNR6_MOUSE
21	166.5	10.8	259	1	T10C_HUMAN
22	162	10.5	241	1	TR18_HUMAN
23	161	10.5	454	1	TR1A_MOUSE
24	160.5	10.4	325	1	VR2_SFVKA
25	152	9.9	326	1	VR2_MXVXL
26	147.5	9.6	324	1	TNR6_RAT
27	147	9.6	595	1	TNR8_HUMAN
28	146.5	9.5	349	1	VC22_VARY
29	145.5	9.4	3110	1	LM42_HUMAN
30	144.5	9.4	260	1	TNR7_HUMAN
31	144.5	9.4	323	1	TNR6_BOVIN
32	144.5	9.4	1581	1	LMG3_MOUSE
33	144	9.4	461	1	TR1A_PIG

34	142	9.2	250	1	TNR7_MOUSE	P41272 mus musculus
35	140	9.1	471	1	TR1A_BOVIN	O19131 bos taurus
36	139	9.0	1587	1	LMG3_HUMAN	O9Y6N6 homo sapien
37	139	9.0	3075	1	LM41_HUMAN	P25391 homo sapien
38	138	9.0	1798	1	LMB2_HUMAN	P35268 homo sapien
39	134	8.7	417	1	TR12_HUMAN	O93038 h wsl-1 pro
40	132	8.6	1801	1	LMB2_RAT	P15800 rattus norv
41	131.5	8.6	332	1	TNR6_PIG	O77736 sus scrofa
42	129.5	8.4	440	1	T10B_HUMAN	O14763 homo sapien
43	129	8.4	1696	1	PK5_BRACL	O9J115 branchiost
44	128.5	8.4	1713	1	LM43_HUMAN	O16787 homo sapien
45	128	8.3	3718	1	LM45_MOUSE	O61001 mus musculus

## ALIGNMENTS

```

RESULT 1
ID      TNR4_HUMAN
AC      P43489; 013663;
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DE      Tumor necrosis factor receptor superfamily member 4 precursor (OX40L
DE      receptor) (ACT35 antigen) (TAX-transcriptionally activated
DE      glycoprotein 1 receptor) (CD134 antigen).
GN      TNFRSF4 OR TNXPIL.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxId=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=94170844; PubMed=7510240;
RA      Latza U., Duerkop H., Schmittiger S., Ringeling J., Etzelbach F.,
RA      Hummel M., Fonatsch C., Stein H.;
RT      "The human OX40 homolog: cDNA structure, expression and chromosomal
RT      assignment of the ACT35 antigen";
RL      Eur. J. Immunol. 24:677-683(1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=95219871; PubMed=7704935;
RA      Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A.,
RA      Watson M.L., Seldin M.F., Clifford K.N., Grabstein K., Alderson M.R.;
RT      "Identification of OX40 ligand and preliminary characterization of
RT      its activation on OX40 receptor";
RL      Cite. Shock 44:30-34(1994).
CC      - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC      - SUBCELLULAR LOCATION: Type I membrane protein.
CC      - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC      - DATABASE: NAME=PROT; NOTE=CD guide CD134 entry;
CC      WWW="http://www.ncbi.nlm.nih.gov/prot/cd/cd134.htm".
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
CC      between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: X75962; CAA53576.1; -
DR      EMBL: S76792; AAB33944.1; ALT_INT.
DR      HSRP: P25942; ICDP.
DR      MIM: 600315; -
DR      InterPro: IPR001368; TNFR_c6.
DR      Pfam: PF00020; TNFR_c6; 3.
DR      ProDom: PD000771; TNFR_c6; 1.
DR      SMART: SM00208; TNFR: 3.
DR      PROSITE: PS00652; TNFR_NGFR_1; 3.
DR      PROSITE: PS50050; TNFR_NGFR_2; 2.
DR      Receptor: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW

```

KM Signal. 1 28 POTENTIAL.  
 FT SIGNAL 29 277 TUMOR NECROSIS FACTOR RECEPTOR  
 FT CHAIN 29 277 SUPERFAMILY MEMBER 4.  
 FT DOMAIN 29 214 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 215 235 POTENTIAL.  
 FT DOMAIN 236 277 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 30 65 TNFR-CYS 1.  
 FT REPEAT 66 107 TNFR-CYS 2.  
 FT REPEAT 108 126 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 127 167 TNFR-CYS 4.  
 FT CAROXYD 146 146 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CAROXYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 277 AA: 29340 MM: 49F13523941350BF CRC64;

Query Match 100.0%; Score 1538; DB 1; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 4, 1e-99;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVGARRLGRPCALLLLGLSTVGLHCVDITYPSNDRCHCECPGNGVSRCSRSQ 60  
 DB 1 MCVGARRLGRPCALLLLGLSTVGLHCVDITYPSNDRCHCECPGNGVSRCSRSQ 60  
 QY 61 NTVCRPCGFGFYNDVSSSRCKPCTWCNLRSGSERKQLCTATQDYCRCRAGTQPIDSYK 120  
 DB 61 NTVCRPCGFGFYNDVSSSRCKPCTWCNLRSGSERKQLCTATQDYCRCRAGTQPIDSYK 120  
 QY 121 PGVDCAFCPPGHFSPDNDACKPMTNCTLAGKHTLQPA SNSDAICEDBDPPATQPEQY 180  
 DB 121 PGVDCAFCPPGHFSPDNDACKPMTNCTLAGKHTLQPA SNSDAICEDBDPPATQPEQY 180  
 QY 181 GPAPRITVQPTPEAMERISQSPSTRPEVPGGNAVALIGLVGLGLPLAILLALYLL 240  
 DB 181 GPAPRITVQPTPEAMERISQSPSTRPEVPGGNAVALIGLVGLGLPLAILLALYLL 240  
 QY 241 RRDRRLPDAHKPPGGSGFRTPIOEQADAHSTLAKI 277  
 DB 241 RRDRRLPDAHKPPGGSGFRTPIOEQADAHSTLAKI 277

RESULT 2  
 TNRA\_RAT STANDARD: PRT: 271 AA.  
 ID TNRA\_RAT  
 AC P15725;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RX MEDLINE=90214614; PubMed=2157591;  
 RA Mallett S., Fossum S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMBO J. 9:1063-1068(1990).  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.

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 CC -----  
 CC EMBL: X17037; CAA34897.1; -  
 DR PIR: S08036; S08036.  
 DR PIR: S12783; S12783.  
 DR HSP: P19438; 1EXT.  
 DR InterPro: IPR001368; TNFR\_C6.  
 DR Pfam: PF00020; TNFR\_C6; 3.  
 DR ProDom: PD000771; TNFR\_C6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR.2; 2.  
 DR Receptor: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL 1 19 POTENTIAL.  
 FT CHAIN 20 271 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 211 235 SUPERFAMILY MEMBER 4.  
 FT DOMAIN 236 271 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 25 60 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 61 102 TNFR-CYS 1.  
 FT REPEAT 103 123 TNFR-CYS 2.  
 FT REPEAT 124 164 TNFR-CYS 3 (INCOMPLETE).  
 FT CAROXYD 143 143 TNFR-CYS 4.  
 SQ SEQUENCE 271 AA: 29895 MM: C06465136B16E821 CRC64;

Query Match 56.2%; Score 864.5; DB 1; Length 271;  
 Best Local Similarity 63.4%; Pred. No. 6, 5e-53;  
 Matches 168; Conservative 18; Mismatches 74; Indels 5; Gaps 3;

QY 15 ALLLLGLSTVGLHCVDITYPSNDRCHCECPGNGVSRCSRSNTVCRCPPGPFYND 74  
 DB 10 AFLLLGLSLGVTVKLVKNCVADITYPSGHCCECPGNGVSRCSRSNTVCRCPPGPFYND 69  
 QY 75 VYSKRCCKPCTWCNLRSGSERKQLCTATQDYCRCRAGTQPL--DSYKGVCAKPPGPH 132  
 DB 70 AVNYDCKCKOCTOCNHRSGSELKQCTPTEDYVCQCRPGTQPRODSSSHKLGVDVCPGPH 129  
 QY 133 FSPGDNDACKPMTNCTLAGKHTLQPA SNSDAICEDBDPPATQPEQY 192  
 DB 130 FSPGSDNDACKPMTNCTLAGKHTLQPA SNSDAICEDBDPPATQPEQY 189  
 QY 193 EAMPTSGSPSTRPEVPGGNAVALIGLVGLGLPLAILLALYLLRRDRLPDAHK 252  
 DB 190 TVMPRTSQSPSTRPEVPGGNAVALIGLVGLGLPLAILLALYLLRRKAWR--SPNTPK 246  
 QY 253 PCWGSFRTPIQEQADAHSTLAKI 277  
 DB 247 PCWGSFRTPIQEQADAHSTLAKI 271

RESULT 3  
 TNRA\_MOUSE STANDARD: PRT: 272 AA.  
 ID TNRA\_MOUSE  
 AC P47741;  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen).  
 GN TNFRSF4 OR TXGP1 OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BALB/C;  
 RX MEDLINE=94044750; PubMed=8228223;  
 RA Calderhead D.M., Buhlmann J.E., van den Beltwegh A.J.,

RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate  
 T-B cell interactions.";  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkehead M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue  
 of rat OX40 protein.";  
 RL Eur. J. Immunol. 23:926-930(1995).  
 CC - FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.  
 CC - SUBCELLULAR LOCATION: Type I membrane protein.  
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
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 CC -----  
 DR EMBL: Z21674; CAA79772.1; -;  
 DR EMBL: X85214; CAA59476.1; -;  
 DR HSSP: P19438; IEXT.  
 DR MGD: MGI:104512; Tnfstf4.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 2.  
 KW Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 KW Signal.  
 FT SIGNAL. 1 19 POTENTIAL.  
 FT CHAIN 20 272 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 20 272 SUPERFAMILY MEMBER 4.  
 FT DOMAIN 20 211 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 212 236 POTENTIAL.  
 FT REPEAT 237 272 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 26 61 TNFR-CYS 1.  
 FT REPEAT 62 103 TNFR-CYS 2.  
 FT REPEAT 104 124 TNFR-CYS 3 (INCOMPLETE).  
 FT REPEAT 125 165 TNFR-CYS 4.  
 FT CARBOHYD 144 144 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 15 15 A -> G (IN REF. 2).  
 SQ SEQUENCE 272 AA; 30153 MW; 06E7BB4156F0D08E CRC64;  
 Query Match 55.7%; Score 857; DB 1; Length 272;  
 Best Local Similarity 63.5%; Pred. No. 2,1e-52;  
 Matches 165; Conservative 20; Mismatches 71; Indels 6; Gaps 4;

DB 247 KPCWGNSTFRPTIOEHTDAHFTLAKI 272  
 RESULT 4  
 ID TNFR3\_MOUSE STANDARD; PRT; 415 AA.  
 AC P50284;  
 DT 01-OCT-1996 (Rel. 34, Created)  
 DT 01-OCT-1996 (Rel. 34, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Lymphotoxin-beta receptor precursor.  
 GN LTR OR TNFRSF3.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090.  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CVB; TISSUE=Lung;  
 RX MEDLINE=96072804; PubMed=7594541;  
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,  
 RA Browning J.L., Ware C.F.;  
 RT "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,  
 RT and expression.";  
 RL J. Immunol. 155:5280-5288(1995).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96163885; PubMed=8586432;  
 RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,  
 RA Honjo T.;  
 RT "The murine lymphotoxin-beta receptor cDNA: isolation by the signal  
 RT sequence trap and chromosomal mapping.";  
 RL Genomics 30:312-319(1995).  
 CC - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN  
 CC IMMUNE DEVELOPMENT.  
 CC - SUBCELLULAR LOCATION: Type I membrane protein.  
 CC - SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: U29173; AAA68864.1; -;  
 DR EMBL: U38423; AAB00846.1; -;  
 DR EMBL: U30798; AAB1334.1; -;  
 DR HSSP: P25942; ICDP.  
 DR MGD: MGI:104875; Ltbr.  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 3.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 3.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
 FT SIGNAL. 1 30 POTENTIAL.  
 FT CHAIN 31 415 LYMPHOTOXIN-BETA RECEPTOR.  
 FT DOMAIN 31 223 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 224 244 POTENTIAL.  
 FT DOMAIN 245 415 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 42 81 TNFR-CYS 1.  
 FT REPEAT 82 124 TNFR-CYS 2.  
 FT REPEAT 125 170 TNFR-CYS 3.  
 FT REPEAT 171 213 TNFR-CYS 4.  
 FT DISULFD 43 58 BY SIMILARITY.  
 FT DISULFD 59 72 BY SIMILARITY.  
 FT DISULFD 62 80 BY SIMILARITY.  
 FT DISULFD 83 98 BY SIMILARITY.  
 FT DISULFD 101 116 BY SIMILARITY.  
 FT DISULFD 104 124 BY SIMILARITY.



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FT VARIANT 13 21 ALLLICALL -> ALLLICALLALLLICALL (IN
FT PDB2).
FT VARIANT 16 21 LICALL -> LICALLALLLICALL (IN PEO).
FT VARIANT 192 192 A -> V.
FT SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 16.1%; Score 247; DB 1; Length 616;
Best Local Similarity 33.3%; Pred. No. 3.1e-10;
Matches 70; Conservative 21; Mismatches 83; Indels 36; Gaps 10;

QY 1 MCVGARRLRGRCALLL-----GLGLSTVGLHCVGDT-YPSNDRCHCRPGNGV 54
D 1 MAPARR--RRPLFALLLICALLRLVALIAPPTSEKHIEHLGRCCNCEPEKYMSS 58
QY 55 RCSRQNTVCRPGCGPFYNDVYSK-PCKPCTWCNL-----RSGSERKOLCTA-- 101
D 59 KCTTSDSVCLPCGPDEYLDNMNEDKCLHKVCDTGKALVAVAGNSTFRRCACGTAGY 118
QY 102 --TDDYVCRCACTQ-----PLDSYKPGVDCAPCPGHPSP--GDNAQCFWNTCT 148
D 119 HWSQDCEC-CHRNTECAPGLGAQHPLQLNKDTV-CKPLAGYFSDAFSSTDKCFWNTCT 176
QY 149 LAGKHTLOPASNSDAICEDRDPRATQPE 178
D 177 FLGKRVEHGHTEKSDAVCSSLPARKPPNE 206

RESULT 6
TR16_HUMAN STANDARD; PRT; 427 AA.
ID TR16_HUMAN
AC P08138;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-AUG-1988 (Rel. 08, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-
DE affinity nerve growth factor receptor) (NGF receptor) (p80-LINGR)
DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).
GN NGFR OR TNFRSF10.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=87051725; PubMed=3022937;
RA Johnson D., Lananan A., Buck C.R., Sehgal A., Morgan C., Mercer E.,
RA Bothwell M., Chao M.;
RT "Expression and structure of the human NGF receptor.";
RL Cell 47:545-554(1986).
RN [2]
RP SEQUENCE OF 1-22 FROM N.A.
RX MEDLINE=89096903; PubMed=2850481;
RA Sehgal A., Patil N., Chao M.;
RT "A constitutive promoter directs expression of the nerve growth factor
RT receptor gene.";
RL Mol. Cell. Biol. 8:3160-3167(1988).
CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,
CC AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF
CC NEURAL CELLS.
CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.
CC INTERACTS WITH P75NTR-ASSOCIATED CELL DEATH EXECUTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
CC -----
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CC -----
CC EMBL: M14764; AAB59544.1; -.
CC EMBL: M21621; AAA36363.1; -.
CC PIR: A25218; GOHUN.
CC HSSP: P07174; INGR.
CC MIM: 162010; -.
DR InterPro: IPR000488; Death.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; death.1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00005; DEATH; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
DR PROSITE: PS50017; DEATH_DOMAIN; 1.
KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
KW Phosphorylation; Signal; Apoptosis.
FT SIGNAL 1 28
FT CHAIN 29 427
FT DOMAIN 29 250 TUMOR NECROSIS FACTOR RECEPTOR
FT TRANSMEM 251 272 SUPERFAMILY MEMBER 16.
FT DOMAIN 273 427 EXTRACELLULAR (POTENTIAL).
FT REPEAT 31 64 CYTOPLASMIC (POTENTIAL).
FT REPEAT 66 107 TNFR-CYS 1.
FT REPEAT 108 146 TNFR-CYS 2.
FT REPEAT 148 188 TNFR-CYS 3.
FT DOMAIN 344 421 TNFR-CYS 4.
FT DOMAIN 197 248 DEATH.
FT DISULFID 32 43 SER/THR-RICH.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 64 BY SIMILARITY.
FT DISULFID 67 83 BY SIMILARITY.
FT DISULFID 86 99 BY SIMILARITY.
FT DISULFID 89 107 BY SIMILARITY.
FT DISULFID 109 122 BY SIMILARITY.
FT DISULFID 125 138 BY SIMILARITY.
FT DISULFID 128 146 BY SIMILARITY.
FT DISULFID 149 164 BY SIMILARITY.
FT DISULFID 167 180 BY SIMILARITY.
FT DISULFID 170 188 BY SIMILARITY.
FT CARBOHD 60 60 N-LINKED (GLCNAc... ) (POTENTIAL).
SO SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 14.6%; Score 224.5; DB 1; Length 427;
Best Local Similarity 30.1%; Pred. No. 7.9e-09;
Matches 84; Conservative 31; Mismatches 95; Indels 69; Gaps 16;

QY 3 VGARRLRG--GP-CAALLILGLL-----STVTGLHCVGDTYPSNDRCHCRPGNGV 53
D 1 MGAGATGRAMGPRLLLLLLLVSLGAKAEAPGL-----YTHSGECKKACNLGEGVA 54
QY 54 SRRCSQNTVCRPGCGPF-YNDVYS-SKPCCKCTWC-NLRSGSERKOLCTATQDYCR-- 108
D 55 QPCGANQ-TVCEPCIDSVTFSDVVSATBCKCTCEVGLQMSAP---CVEADAVVCRA 110
QY 109 -----CRAGTQPLDSY--KRGVCAAPCPGHPSPGDNA--CKPWTNC 147
D 111 YGYDDETTCGCEACRVCEAGSLVFCODKONTVCCECPDGTSDDEAHNVDPCLPCTYC 170
QY 148 TLGKHTLOPASNSDAICED-----RDPATQPEOTGPPARPITVQPTPE 193
D 171 E-DTRQLRECTRMADABEELPGRMVTRSPPEGSDSAPSTQPEAPPEQDL-IASIV 228
QY 194 AMPRTSQGPSTRPVE-----VPGRAVVAAILLGLGLV 224
D 229 AGVVTVMGSSQPVVTRGTDTNLLIPVYCSIIAAVVVGLV 267
```



RESULT 7  
 TNRS\_HUMAN STANDARD: PRT: 277 AA.  
 ID TNRS\_HUMAN  
 AC P25942:  
 DT 01-MAR-1992 (Rel. 22, Created)  
 DT 01-MAY-1992 (Rel. 22, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 5 precursor  
 DE (CD40L receptor) (B-cell surface antigen CD40) (Bp50) (CD40).  
 GN TNFRSF5 OR CD40.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 (1)  
 RP MEDLINE=89356608; PubMed=2475341;  
 RA Stamenkovic I., Clark E.A., Seed B.;  
 RT "A B-lymphocyte activation molecule related to the nerve growth  
 RT factor receptor and induced by cytokines in carcinomas.";  
 RL EMBO J. 8:1403-1410(1989).  
 (2)  
 RP SEQUENCE FROM N.A.  
 RA Deloukas P., Matthews L.H., Ashurst J., Burton J., Gilbert J.G.R.,  
 RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,  
 RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,  
 RA Beasley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,  
 RA Buck D., Burrill W., Butler A.P., Carder C., Carter N.P., Clee C.M.,  
 RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,  
 RA Cligg S., Cobley V.E., Collier R.E., Connor R., Corby N.R.,  
 RA Coulson A., Coville G.J., Deadman R., Dhami P., Dunn M.,  
 RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,  
 RA Graham D.V., Griffiths C., Griffiths M.N.D., Gilliam R., Hall R.E.,  
 RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,  
 RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,  
 RA Kay M.P., Kimberley A.M., King A., Knights A., Laird G.K., Lawlor S.,  
 RA Levasalho M.H., Leversha M., Lloyd C., Lloyd D.M., Lovell J.D.,  
 RA Marsh V.L., Martin S.L., McConachie L.J., McLeay K., Murray A.A.,  
 RA Milne S., Mistry D., Moore M.J.F., Mullikin J.C., Nickerson T.,  
 RA Oliver K., Parker A., Patel R., Pearce T.A.V., Peck A.I.,  
 RA Phillimore B.J.C.T., Prithalingam S.R., Plumb R.W., Ramsay H.,  
 RA Rice C.M., Ross M.T., Scott C.E., Senta H.K., Showkeen R., Sims S.,  
 RA Skuce C.D., Smith M.L., Soderlund C., Steward C.A., Sulston J.E.,  
 RA Swann M., Symcox N., Taylor R., Tee L., Thomas D.W., Thorpe A.,  
 RA Tracey A., Tromans A.C., Vaudin M., Wall M., Wallis J.M.,  
 RA Whitehead S.L., Whitaker P., Willey D.L., Williams L., Williams S.A.,  
 RA Wilmshurst L., Wray P.W., Hubbard T., Durbin R.M., Bentley D.R., Beck S.,  
 RA Rogers J.;  
 RT "The DNA sequence and comparative analysis of human chromosome 20.";  
 RL Nature 414:865-871(2001).  
 (3)  
 RP 3D-STRUCTURE MODELING OF 24-144.  
 RX MEDLINE=97189482; PubMed=9037712;  
 RT Bajorath J., Aruffo A.;  
 RT "Construction and analysis of a detailed three-dimensional model of  
 RT the 15and-binding domain of the human B cell receptor CD40.";  
 RL Proteins 27:59-70(1997).  
 (4)  
 RP 3D-STRUCTURE MODELING OF 26-186 IN COMPLEX WITH CD40L.  
 RX MEDLINE=9826353; PubMed=9605317;  
 RA Singh J., Garner E., van Vlijmen H., Karpusas M., Hsu Y.-M.,  
 RA Zheng Z., Naismith J.H., Thomas D.;  
 RT "The role of polar interactions in the molecular recognition of CD40L  
 RT with its receptor CD40.";  
 RL Protein Sci. 7:1124-1135(1998).  
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
 CC -1- SUBCELLULAR LOCATION: type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- DATABASE: NAME=PROW; NOTE=CD guide CD40 entry;  
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd40.htm".

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 CC -----  
 DR EMBL: X60592; CAA43045.1; -  
 DR EMBL: AL035662; CAC14670.1; -  
 DR PIR: S04460; S04460  
 DR PDB: ICDF; 01-APR-97.  
 DR MIM: 109535; -  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00552; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;  
 KW 3D-structure.  
 FT SIGNAL 1 19  
 FT CHAIN 20 277  
 FT DOMAIN 20 193  
 FT TRANSMEM 194 215  
 FT DOMAIN 216 277  
 FT REPEAT 25 60  
 FT REPEAT 61 103  
 FT REPEAT 104 144  
 FT REPEAT 145 187  
 FT DISULFID 26 37  
 FT DISULFID 38 51  
 FT DISULFID 41 59  
 FT DISULFID 62 77  
 FT DISULFID 83 103  
 FT DISULFID 105 119  
 FT DISULFID 111 116  
 FT DISULFID 125 143  
 FT CARBOHYD 153 153  
 FT CARBOHYD 180 180  
 SQ SEQUENCE 277 AA; 30619 MW; BC8776BC2C4A5680 CRC64;  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 N-LINKED (GLCNAC... ) (POTENTIAL).  
 Query Match 14.4%; Score 221.5; DB 1; Length 277;  
 Best Local Similarity 23.2%; Pred. No. 8.7e-09;  
 Matches 66; Conservative 34; Mismatches 95; Indels 89; Gaps 10;  
 QY 26 VYGLH-----CYGDYPSNDRCCHCRGNGVNSRCSQNTVCRPCGFGFYNDVYSSK 79  
 DB 15 LTAHPEPTPACREKQYLINSQCSLCPQKLVSDCTETETECCLPCGSEPLDWNRE 74  
 QY 80 P-CRPTWNCNLRSRERKOLCTATOPTVCRCRAGTGPLD-----SYKPGVD---- 124  
 DB 75 THCHQKRYCDPNGLGVQKGTSETDTICGEGNHCSTACSVLHRCSGPGVKOI 134  
 QY 125 -----CAPCPGHPSPGDN--QACKPWTNCTLAGKHTLPASNSDAICSDRPPAT 174  
 DB 135 ATGVSDTICEPCVGFESNVSFAFEKCHPWTSCETKDLVVOAGCTKKTVDVC----- 186  
 QY 175 QPQETGPPRRPRTTVQPTQTEAMPRTSOGPSRPRPEVNGRVAVALIGLVGLGLPLAIL 234  
 DB 187 -----GPDOR-----LRALVPIPIIFGL--FALL 209  
 QY 235 LALYLRLRDORLP-----PDANKRP-----GGGSFRTPIOE 265  
 DB 210 LVLVFTKKYAKKPTNKAPHPKQEPQELNFPDDLPGSTAPAYOE 253  
 RESULT 8  
 ID TRIL\_MOUSE  
 AC 035305; STANDARD: PRT: 625 AA.

DT 16-OCT-2001 (Rel. 40, Created)  
 DT 16-OCT-2001 (Rel. 40, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 11A precursor  
 DE (receptor activator of NF-kB) (osteoclast differentiation factor  
 DE receptor) (ODFR).  
 GN TNFRSF11A OR RANK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Fetal liver;  
 RX MEDLINE=98032977; PubMed=9367155;  
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,  
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,  
 RA Galibert L.;  
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth  
 RT and dendritic-cell function.";  
 RL Nature 390:175-179(1997).  
 RN [2]  
 RP FUNCTION  
 RX MEDLINE=99097247; PubMed=9878548;  
 RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,  
 RA Morinaga T., Higashio K.;  
 RT "RANK is the essential signaling receptor for osteoclast  
 RT Biochem. Biophys. Res. Commun. 253:395-400(1998).  
 RL [1]  
 CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL), ALSO KNOWN AS  
 CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-  
 CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF  
 CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).  
 CC -1- TISSUE SPECIFICITY: UBQUITOUS EXPRESSION WITH HIGH LEVELS IN  
 CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.  
 CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -----  
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 CC -----  
 DR EMBL: AF019046; AAB86810.1; -;  
 DR HSSP: P25942; ICDF.  
 DR MGD: MGI:1314891; Tnftrsf11a.  
 DR InterPro: IPR001368; TNFR\_C6.  
 DR Pfam: PF000020; TNFR\_C6; 3.  
 DR PRODOM: PD000771; TNFR\_C6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 1.  
 KM Receptor: Glycoprotein; Transmembrane: Repeat; Signal.  
 FT SIGNAL 1 30  
 FT CHAIN 31 625  
 FT TUMOR NECROSIS FACTOR RECEPTOR  
 FT SUPERFAMILY MEMBER 11A.  
 FT EXTRACELLULAR (POTENTIAL).  
 FT POTENTIAL.  
 FT CYTOPLASMIC (POTENTIAL).  
 FT TNFR-CYS 1.  
 FT REPEAT 72 113  
 FT REPEAT 115 152  
 FT REPEAT 155 195  
 FT REPEAT 195 47  
 FT REPEAT 48 61  
 FT REPEAT 61 69  
 FT REPEAT 69 87  
 FT REPEAT 87 113  
 FT REPEAT 113 128  
 FT REPEAT 128 115  
 FT REPEAT 115 128

FT DISULFID 134 152 BY SIMILARITY.  
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SO SEQUENCE 625 AA; 66621 MM; F8C1872E95911DBE CRC64;  
 Query Match 14.4%; Score 221.5; DB 1; Length 625;  
 Best Local Similarity 30.3%; Pred. No. 1.8e-08;  
 Matches 67; Conservative 17; Mismatches 84; Indels 53; Gaps 10;  
 QY 1 MCVGARRLRGPCAAAL-----LLILGLSTVYGLHCVGT-YPNSDRCCHECPNGMYSR 55  
 DB 1 MAPRARRRROLPAPLALCVLLVPLQVTPPTCTOERHYEHLRCCSRCEPGRYLSK 60  
 QY 56 CSRSNTWCRCPCGPGFYNDVVSRSKRCRCCTM-----CNLRS-----GSE 94  
 DB 61 CTPISDSVCLPCGPDEYLD-----TNWEDKCLLHKYCDAGKALVAADPGNHTAP 110  
 QY 95 RKOLCTA---TODVCRCRAGTQ-----PLDSYKPGVDCAPCPGHFSP--GDNO 139  
 DB 111 RRCACIAGYHNNSDCEC-CRRTTECAPGFGAHPQLKNDIV-CIPCLLGFPSDFSSSTD 168  
 QY 140 ACKPWTNCTLAGKHTLPASNSSDAICEDRDPATQPEETQ 180  
 DB 169 KCKPWTNCTLGLKEAHOGTTESDVCSSMTLRPRPEAQ 209  
 RESULT 9  
 TRIB\_HUMAN STANDARD; PRT; 461 AA.  
 ID TRIB\_HUMAN  
 AC P20333;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-AUG-1991 (Rel. 19, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor 2 precursor (Tumor necrosis factor  
 DE binding protein 2) (TBPI1) (p60) (TNF-R2) (P75) (CD120b) (Ectanrecept).  
 GN TNFRSF1B OR TNFR2 OR TNFR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90260639; PubMed=2160731;  
 RA Smith C.A., Davis T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,  
 RA Dower S.K., Cosman D., Goodwin R.G.;  
 RT "A receptor for tumor necrosis factor defines an unusual family of  
 RT cellular and viral proteins.";  
 RL Science 248:1019-1023(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91045991; PubMed=2172983;  
 RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,  
 RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;  
 RT "A second tumor necrosis factor receptor gene product can shed a  
 RT naturally occurring tumor necrosis factor inhibitor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=96299745; PubMed=8661109;  
 RA Bellingier C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,  
 RA Lepeslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.;  
 RT Broder G.M.;  
 RL "Physical mapping and genomic structure of the human TNFR2 gene.";  
 RN Genomics 35:94-100(1996).  
 RN [4]  
 RP SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.  
 RX MEDLINE=90349572; PubMed=2166946;  
 RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,  
 RA Ringold G.M.;  
 RT "Complementary DNA cloning of a receptor for tumor necrosis factor  
 RT and demonstration of a shed form of the receptor.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).

RN [5]  
 RP SEQUENCE OF 27-31.  
 RX MEDLINE-90110215; PubMed-2153136;  
 RA Engelmann H., Novick D., Wallach D.;  
 RT "Two tumor necrosis factor-binding proteins purified from human  
 RT urine. Evidence for immunological cross-reactivity with cell surface  
 RT tumor necrosis factor receptors";  
 RL J. Biol. Chem. 265:1531-1536(1990).  
 RN [6]  
 RP SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.  
 RX MEDLINE-91056048; PubMed-2173696;  
 RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,  
 RA Brockhaus M.;  
 RT "Purification and partial amino acid sequence analysis of two  
 RT distinct tumor necrosis factor receptors from HL60 cells.";  
 RL J. Biol. Chem. 265:20131-20138(1990).  
 RN [7]  
 RP CHARACTERIZATION.  
 RX MEDLINE-93016040; PubMed-1328224;  
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,  
 RA Lipari M.T., Goeddel D.V.;  
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.  
 RT Characterization of ligand binding, internalization, and receptor  
 RT phosphorylation";  
 RL J. Biol. Chem. 267:21172-21178(1992).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH  
 RP TRAF2.  
 RX MEDLINE-99221490; PubMed-10206649;  
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;  
 RT "Structural basis for self-association and receptor recognition of  
 RT human TRAF2";  
 RL Nature 398:533-538(1999).  
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND  
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- PTM: PHOSPHORYLATED: MAINLY ON SERINE RESIDUES WITH A VERY LOW  
 CC LEVEL ON THREONINE RESIDUES.  
 CC -1- PHARMACEUTICAL: Available under the name Embrel (Immunex and  
 CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid  
 CC arthritis (RA). Embrel consist of the extracellular ligand-binding  
 CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to  
 CC TNF-alpha and blocks its interactions with receptors.  
 CC -1- SIMILARITY: CONTRAINS 4 TNFR-CYS REPEATS.  
 CC -1- DATABASE: NAME-PROW; NOTE-CD guide CD120b entry;  
 CC WWW-"http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".  
 CC -1- DATABASE: NAME-Embrel; NOTE-Clinical information on Embrel;  
 CC WWW-"http://www.embrelinfo.com/".  
 CC -----  
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 CC -----  
 DR EMBL: M32315; AA55929.1; -;  
 DR EMBL: M35857; AAA63262.1; -;  
 DR EMBL: U52165; AAC50622.1; JOINED.  
 DR EMBL: U52156; AAC50622.1; JOINED.  
 DR EMBL: U52157; AAC50622.1; JOINED.  
 DR EMBL: U52158; AAC50622.1; JOINED.  
 DR EMBL: U52159; AAC50622.1; JOINED.  
 DR EMBL: U52160; AAC50622.1; JOINED.  
 DR EMBL: U52161; AAC50622.1; JOINED.  
 DR EMBL: U52162; AAC50622.1; JOINED.  
 DR EMBL: U52163; AAC50622.1; JOINED.  
 DR EMBL: U52164; AAC50622.1; JOINED.  
 DR EMBL: M55994; AAA36755.1; -;  
 DR PIR: A35356; A35356.  
 DR PIR: A36007; A36007.  
 DR PIR: A36475; A36475.

DR PIR: B35010; B35010.  
 DR PIR: A23666; A23666.  
 DR PDB: 1CA9; 12-APR-99.  
 DR MIM: 191191; -;  
 DR InterPro: IPR001368; TNFR\_c6.  
 DR Pfam: PF00020; TNFR\_c6; 4.  
 DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART: SM00208; TNFR; 4.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
 DR PROSITE: PS00505; TNFR\_NGFR\_2; 4.  
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;  
 KW Phosphorylation; Pharmaceutical; 3D-structure.  
 FT SIGNAL 1 22  
 FT CHAIN 23 461  
 FT DOMAIN 23 257  
 FT TRANSMEM 288 287  
 FT DOMAIN 288 461  
 FT REPEAT 39 76  
 FT REPEAT 77 118  
 FT REPEAT 119 162  
 FT REPEAT 163 201  
 FT DISULFID 40 53  
 FT DISULFID 54 67  
 FT DISULFID 57 75  
 FT DISULFID 78 93  
 FT DISULFID 96 110  
 FT DISULFID 100 118  
 FT DISULFID 120 126  
 FT DISULFID 134 143  
 FT DISULFID 137 161  
 FT DISULFID 164 179  
 FT CARBOHYD 171 171  
 FT CARBOHYD 193 193  
 FT CONFLICT 141 141  
 FT CONFLICT 196 196  
 FT CONFLICT 363 363  
 SQ SEQUENCE 461 AA; 48316 MW; 603B580ECD67636F CRC64;  
  
 Query Match 14.1%; Score 217; DB 1; Length 461;  
 Best Local Similarity 26.0%; Pred. No. 2.8e-08;  
 Matches 74; Conservative 29; Mismatches 108; Indels 74; Gaps 13;  
  
 QY 12 PCAALLLLGLGSLTVGLGCV-----GPTV-----PSNDRCHCEKPGNG 51  
 DB 3 PAVAWMAALVAGELMAAALPAQAFAETPAPEPGSTCYLREYDDTAQMCCSKSPGQH 62  
 QY 52 MVSRCRSQNTVCRPCGPGFYNDVSSKPCCKPCTWNLRSQSPR--KQLCTATQDTVCRC 109  
 DB 63 AKVFCTKTSPTYDSCEDSDSTYQLNMWVP--ELSCGSKSSDQVETQACTREONRICTC 120  
 QY 110 RAG-----TOPLDSTYKPG-----VDCAPCPGHS--PGDNQACK 142  
 DB 121 RGVWCALSKQECRCALRCRCRPGFVARPQETETSDVCKRCACGTFSTNTSSTDICR 180  
 QY 143 PPTNCTLAKHTLQPAASNSDAICEDRDPAPQPOQTQGPRA---RPTTV--QPTFEMP 196  
 DB 181 PHQICNVVA---IPGNASRDVAC---TSTPSRSMAPGAVNLPQVSTNSQHTQPPR 231  
 QY 197 RTSQGPSTR-----PVEVPGRAVAAILGLGLVLG--LGPLAI 233  
 DB 232 EPSTAPSTSFLLPMGSPPAEGSTGDFALPVLGLVGTALGLIIT 276  
  
 RESULT 10  
 TR16\_RAT STANDARD; PRT; 425 AA.  
 ID TR16\_RAT  
 AC P07174;  
 DT 01-APR-1988 (Rel. 07, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-  
 DE affinity nerve growth factor receptor) (NGF receptor) (Gp80-LNGFR)

(p75 ICD) (low affinity neurotrophin receptor p75NTR).  
 NGFR OR TNFRSF16.  
 OS Rattus norvegicus (Rat).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Mammalia; Euteleostomi; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 RX NCBI\_TaxID=10116;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RX MEDLINE=6711589; PubMed=1027580;  
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;  
 RT "gene transfer and molecular cloning of the rat nerve growth factor  
 receptor.";  
 RL Nature 325:593-597(1987).  
 RN [2]  
 RN SEQUENCE OF 1-22 FROM N.A.  
 RC TISSUE=Liver;  
 RX MEDLINE=93077038; PubMed=1446821;  
 RA Metts M., Timmusk T., Allikmets R., Saarma M., Persson H.;  
 RT "Regulatory elements and transcriptional regulation by testosterone  
 and retinoic acid of the rat nerve growth factor receptor promoter.";  
 RL Gene 121:247-254(1992).  
 RN [3]  
 RN STRUCTURE BY NMR OF 334-418.  
 RX MEDLINE=97449145; PubMed=9305641;  
 RA Lieplish E., Ilag L.L., Oetting G., Ibanez C.F.;  
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";  
 RL EMBL J. 16:4999-5005(1997).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,  
 AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF  
 NEURAL CELLS.  
 CC -1- SUBUNIT: CAN FORM A HOMODIMER THROUGH DISULFIDE BOND FORMATION.  
 CC -1- SUBCELLULAR LOCATION: TYPE I membrane protein.  
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL: X05137; CAA28783.1; -;  
 DR EMBL: X61269; -; NOT\_ANNOTATED\_CDS.  
 DR PIR: A26431; A26431.  
 DR PDB: 1NGR; 29-JUL-97.  
 DR InterPro: IPR000488; Death.  
 DR InterPro: IPR001368; TNFR\_C6.  
 DR Pfam: PF00531; death; 1.  
 DR Pfam: PF00020; TNFR\_C6; 4.  
 DR SMART: SM00005; DEATH; 1.  
 DR SMART: SM00208; TNFR; 3.  
 DR PROSITE: PS00652; TNFR\_NGFR\_1; 3.  
 DR PROSITE: PS50050; TNFR\_NGFR\_2; 4.  
 DR PROSITE: PS50017; DEATH\_DOMAIN; 1.  
 KM Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;  
 KM Phosphorylation; Signal; Apoptosis; 3D-structure.  
 FT SIGNAL 1 29  
 FT CHAIN 30 425  
 FT  
 FT DOMAIN 30 251 TUMOR NECROSIS FACTOR RECEPTOR  
 FT TRANSMEM 252 273 SUPERFAMILY MEMBER 16.  
 FT DOMAIN 274 425 EXTRACELLULAR (POTENTIAL).  
 FT REPEAT 32 65 CYTOPLASMIC (POTENTIAL).  
 FT REPEAT 67 106 TNFR-CYS 1.  
 FT REPEAT 109 147 TNFR-CYS 2.  
 FT REPEAT 149 189 TNFR-CYS 3.  
 FT DOMAIN 354 419 TNFR-CYS 4.  
 FT DOMAIN 198 249 DEATH.  
 FT DISULFID 33 44 SER/THR-RICH.  
 FT DISULFID 45 58 BY SIMILARITY.  
 FT BY SIMILARITY.

FT DISULFID 48 65 BY SIMILARITY.  
 FT DISULFID 68 84 BY SIMILARITY.  
 FT DISULFID 87 100 BY SIMILARITY.  
 FT DISULFID 90 108 BY SIMILARITY.  
 FT DISULFID 110 123 BY SIMILARITY.  
 FT DISULFID 126 139 BY SIMILARITY.  
 FT DISULFID 129 147 BY SIMILARITY.  
 FT DISULFID 150 165 BY SIMILARITY.  
 FT DISULFID 168 181 BY SIMILARITY.  
 FT DISULFID 171 189 BY SIMILARITY.  
 FT CARBOHYD 61 61 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 71 71 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D94D3827F8 CRC64;  
 Query Match 14.08; Score 216; DB 1; Length 425;  
 Best Local Similarity 29.68; Pred. No. 3e-08;  
 Matches 83; Conservative 29; Mismatches 94; Indels 74; Gaps 15;  
 QY 6 RRLGPGCAA-----LLLLGLGLST-----VTGLHCYGDTPPSNDRCCHECRPGNGM 52  
 Db 2 RRAG-AACSAADRLLRLLLLLVSSGCAKETCTGL-----YHSECCCKACNLGEGV 54  
 QY 53 VSRCSRQNTVCRCPCGPGF-YNDVVS-SKPCPKTCWC-NLNSGERRKOLCTATDPTVCRC 109  
 Db 55 AOPCGANG-TVCEPCLDNVTFSDVVSATEPCKPCTECGLGMSAP--CYEADAVACRC 110  
 QY 110 RAGTQPLDST-----KPYDCAKPCPGHSPGDNOA--CKPWTN 146  
 Db 111 AVGYQDETHGHCACVCEVSGSLVFCODKNTVCCECEGTSDANHVDPCLPCTV 170  
 QY 147 CTLAGKHTLOPASNSDAICED-----RPPPTQPOETGPPAPRTVQPT 192  
 Db 171 CE-DTERLRRECTPMADCEIEFERMTIPRSTPPGSGSTAPSTQDEPVEPQDL-VST 228  
 QY 193 EAMPRTSQGPSTPYE-----VPGGRAVAAILGLGLV 224  
 Db 229 VADWTTVMGSSOPVYRTGTDTNLIPVCSILAAVVGLV 268  
 RESULT 11  
 TR16.CHICK STANDARD; PRT; 416 AA.  
 AC TR16.CHICK  
 ID P18519;  
 DT 01-NOV-1990 (Rel. 16, Created)  
 DT 01-NOV-1990 (Rel. 16, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 16 precursor (Low-  
 affinity nerve growth factor receptor) (NGF receptor) (gp80-LNGFR)  
 DE (p75 ICD) (Low affinity neurotrophin receptor p75NTR).  
 GN NGFR OR TNFRSF16.  
 OS Gallus gallus (chicken).  
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
 CC Gallus.  
 RX NCBI\_TaxID=9031;  
 RN [1]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Brain;  
 RX MEDLINE=90166579; PubMed=2560385;  
 RA Large T.H., Weskamp G., Heider J.C., Radeke M.J., Misko T.P.,  
 RA Shooter E.M., Reichardt L.F.;  
 RT "Structure and developmental expression of the nerve growth factor  
 receptor in the chicken central nervous system.";  
 RL Neuron 2:1123-1134(1989).  
 RN [2]  
 RN SEQUENCE OF 21-416 FROM N.A.  
 RX MEDLINE=90152140; PubMed=2154393;  
 RA Heuer J.G., Fatemie-Nainie S., Wheeler E.F., Bothwell M.;  
 RT "Structure and developmental expression of the chicken NGF receptor.";  
 RL Dev. Biol. 137:287-304(1990).  
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF, NT-3,  
 AND NT-4. CAN MEDIATE CELL SURVIVAL AS WELL AS CELL DEATH OF



FT DISULFID 142 167 BY SIMILARITY.  
FT DISULFID 170 185 BY SIMILARITY.  
FT CARBOHYD 40 40 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 177 177 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 435 AA; 46709 MW; 6246268022P656F CRC64;

Query Match 13.6%; Score 209.5; DB 1; Length 435;  
Best Local Similarity 24.5%; Pred. No. 8.6e-08;  
Matches 67; Conservative 27; Mismatches 87; Indels 93; Gaps 9;

QY 37 PSNDRCHECRPGNGMVSRCRSRONTVCRCGPGFYNDVSSKCPKPTWCNLRSGSER 95  
D 53 POHRICSRCPGTYVSAKSRIRDTWCALCAENSYNENMYLTIQICRCPDPMGLEE 112  
QY 96 KQCTATQDPTVCRCRAG-----TQPLDSYKRGVD-----CAPCP 130  
D 113 IAPCTBRKRTQCRQCPGFCAAMALECTHCLLSDCPGTEALKEDEYKGNHNCVPCKA 172  
QY 131 GHF--SPGDNOACKPWTNCTLAGKHTLPASNSSDAICEDRDPATOPQETGPPARPIT 188  
D 173 GHFQNTSPSARQCPHTRCEMGLVEAPRAGSDTICKN-----PLEPL- 217  
QY 189 VQPTAMPRTSQGPSTRPEVYVGRRAVAAILGLVLGLGPLAIAL----- 237  
D 218 -----PPEMSGTM-----LMLAVLLPLAFLLLATVFCIMKSH 251  
QY 238 -----YLLRRDQRLPPDAHKPPGGSPFRTP 262  
D 252 PSICRKLGLSLKRRPQGEPPN---PVAGSWEPP 281

## RESULT 13

TNR9\_MOUSE  
ID TNR9\_MOUSE STANDARD; PRT; 289 AA.  
AC P27312;  
DT 01-AUG-1992 (Rel. 23, Created)  
DT 01-OCT-1996 (Rel. 34, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Tumor necrosis factor receptor superfamily member 5 precursor  
(CD40L receptor) (B-cell surface antigen CD40) (BP50) (CDW40).  
GN TNR95 OR CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;

RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92105763; PubMed=1370315;  
RA Torres R.M., Clark E.A.;  
RT "Differential increase of an alternatively polyadenylated mRNA  
RT species of murine CD40 upon B lymphocyte activation.";  
RL J. Immunol. 148:620-626(1992).  
RN [2]  
RP REVISIONS.  
RC STRAIN-BALB/C;  
RA Torres R.M.;  
RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.

RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-BALB/C; TISSUE=Liver;  
RX MEDLINE=93094586; PubMed=1281194;  
RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,  
RA Howard M., Cockayne D.A.;  
RT "Genomic structure and chromosomal mapping of the murine CD40 gene.";  
RL J. Immunol. 149:3921-3926(1992).  
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.  
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
CC -1- SIMILARITY: CONTAINS 4 TNR9-CYS REPEATS.

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CC EMBL; M83312; AAB08705.1; -;  
DR EMBL; M94126; AAA37404.1; -;  
DR EMBL; M94129; AAA37404.1; JOINED.  
DR EMBL; M94128; AAA37404.1; JOINED.  
DR EMBL; M94127; AAA37404.1; JOINED.  
DR PIR; A46476; A46476.  
DR HSSP; P25942; IGDF.  
DR MGD; MGI:88336; Tnfrsf5.  
DR InterPro; IPR001368; TNR\_C6.  
DR Pfam; PF00020; TNR\_C6; 4.  
DR ProDom; PD000771; TNR\_C6; 1.  
DR SMART; SM00208; TNR; 4.  
DR PROSITE; PS00652; TNR\_NGFR\_1; 1.  
DR PROSITE; PS00650; TNR\_NGFR\_2; 4.  
KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.  
FT SIGNAL 1 19  
FT CHAIN 20 289  
FT DOMAIN 20 193  
FT TRANSMEM 194 215  
FT DOMAIN 216 289  
FT REPEAT 25 60  
FT REPEAT 61 103  
FT REPEAT 104 144  
FT REPEAT 145 187  
FT DISULFID 26 37  
FT DISULFID 38 51  
FT DISULFID 41 59  
FT DISULFID 62 77  
FT DISULFID 83 103  
FT DISULFID 105 119  
FT DISULFID 111 116  
FT DISULFID 125 143  
FT CARBOHYD 153 153  
FT SEQUENCE 289 AA; 32111 MW; C791CB6D2FEA57AE CRC64;

Query Match 13.6%; Score 209; DB 1; Length 289;  
Best Local Similarity 22.0%; Pred. No. 6.5e-08;  
Matches 64; Conservative 39; Mismatches 96; Indels 92; Gaps 9;

QY 26 VTGLH-----CVGDTYSNDRCHCECRPGNGMVSRCRSRONTVCRCGPGFYNDVSSK 79  
D 15 LTAVALGOCVYTCSDKQYLHDGQCCDLCPGSRITSHCTALEKTQCHPCDSGEFSQMWRE 74  
QY 80 -PKRPTWCNLRSGSERKQCTATQDPTVCRCRAG----- 112  
D 75 IRCHORHRCPEPNOGLRVKKEGTAEBSDTVCTCEGCHCTSKDEACAGTPTCLPGGVNEM 134  
QY 113 -TOPLDYKPGVDCAPCEPGHSPGDNOA-----CKPWTNCTLAGKHTLPASNSSDAIC 166  
D 135 ATETTDIV-----CHPCVGVGFS---NQSLEKCYPTWSCBDKMLEVLQKGTSTPTNYIC 186  
QY 167 EDRDPATQPOETGPPARPITVQPTAMPRTSQGPSTRPEVYVGRRAVAAILGLGLVLG 226  
D 187 -----GLKSR-----MRALLVLPVWG 203  
QY 227 LGLPLAIALYLLRRDQRLPPDAHKPPGGSPFRPIEGQADASTLAKI 277  
D 204 IL--ITITGVFLYIKKVKKPKDNEMLPAPARRQDPQEMEDYPGHNTAPV 252

## RESULT 14

ID TNR9\_MOUSE STANDARD; PRT; 256 AA.  
AC P20334;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-FEB-1991 (Rel. 17, Last sequence update)





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or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).

DR EMBL; M60469; AAA39752.1; -;  
DR EMBL; M59378; AAA40463.1; -;  
DR EMBL; U39488; AAA85021.1; -;  
DR EMBL; X87128; CAA60618.1; -;  
DR PIR; B38634; B38634.  
DR HSSP; P19438; 1NCF.  
DR MGD; MGI:131483; Tfrsflb.  
DR InterPro; IPR001368; TNFR\_c6.  
DR Pfam; PF00020; TNFR\_c6; 4.  
DR ProDom; PD000771; TNFR\_c6; 1.  
DR SMART; SM00208; TNFR; 4.  
DR PROSITE; PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE; PS50050; TNFR\_NGFR\_2; 3.  
KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.  
FT SIGNAL 1 22  
FT CHAIN 23 474 TUMOR NECROSIS FACTOR RECEPTOR 2.  
FT DOMAIN 23 258 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 259 288 POTENTIAL.  
FT DOMAIN 289 474 CYTOPLASMIC (POTENTIAL).  
FT REPEAT 39 77 TNFR-CYS 1.  
FT REPEAT 78 119 TNFR-CYS 2.  
FT REPEAT 120 164 TNFR-CYS 3.  
FT REPEAT 165 203 TNFR-CYS 4.  
FT DISULFID 40 54 BY SIMILARITY.  
FT DISULFID 55 68 BY SIMILARITY.  
FT DISULFID 58 76 BY SIMILARITY.  
FT DISULFID 79 94 BY SIMILARITY.  
FT DISULFID 97 111 BY SIMILARITY.  
FT DISULFID 101 119 BY SIMILARITY.  
FT DISULFID 121 127 BY SIMILARITY.  
FT DISULFID 136 145 BY SIMILARITY.  
FT DISULFID 139 163 BY SIMILARITY.  
FT DISULFID 166 181 BY SIMILARITY.  
FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SO SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;

Query Match 13.2%; Score 202.5; DB 1; Length 474;  
Best Local Similarity 25.1%; Pred. No. 2.8e-07;  
Matches 68; Conservative 36; Mismatches 86; Indels 81; Gaps 14;

QY 42 CCHCRPENGWVSRCSRQNTVCRRCGFGFYNDVYSKPKRCPTWCNLRSGSERKOL--C 99  
DB 54 CCACCPPEQYVYKHFCKNTKSTDTVCADCEASMTQVWNO--FRTCLSCSSCTTDQVEIRAC 111  
QY 100 TATQDTVCRCRAG-----TQPLDSYKPG-----VDCAPCPGHE 133  
DB 112 TKQGNRVACACGARGCALKTHSGSCROCMRLSKCPGFGVASSRAPNGNVLCACAPGTF 171  
QY 134 S--PEDNOACKPWTNCTLAGKHTLQPASNSSDAICEDRP----PAT---QPOETGCP 182  
DB 172 SDTTSSTDVYCRPHRICSLIA----IPGNASTDVCAPESPILSAIPRTLYVSQPEPTRS- 226  
QY 183 PARPTVOPTTEAMPTSGPS-----TRPV---EVPGRANAATLIGIVIGLIGLPLAI 233  
DB 227 -----QPLDQEPGSPQPTSLTSLGSPITIBOSTKGGIS---LPIGLIVGVSGLIL 275  
QY 234 LIALY-----LLRDRLP--PD 249  
DB 276 MLGLVNCITIVQRKKKPSCLQBDAAVPHVPD 306

Search completed: June 18, 2002, 14:28:29  
Job time: 223 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: June 18, 2002, 14:24:01 ; Search time 26.53 Seconds  
(without alignments)  
1806.242 Million cell updates/sec

Title: US-09-852-845-2  
Perfect score: 1538  
Sequence: 1 MCVGARRLRGPCALLLLG.....SFRTPIOEADAHSTLAKI 277

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

## Database :

SPREMBL\_19:\*  
1: sp\_archaea:\*  
2: sp\_bacteria:\*  
3: sp\_fungi:\*  
4: sp\_human:\*  
5: sp\_invertebrate:\*  
6: sp\_mammal:\*  
7: sp\_mhc:\*  
8: sp\_organelle:\*  
9: sp\_phage:\*  
10: sp\_plant:\*  
11: sp\_protent:\*  
12: sp\_virus:\*  
13: sp\_vertebrate:\*  
14: sp\_unclassified:\*  
15: sp\_rvirus:\*  
16: sp\_bacteriap:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	924	60.1	267	6 002764	002764 oryctolagus
2	229.5	14.9	276	13 09DD2	09dd22 gallus galli
3	226	14.7	300	4 095407	095407 homo sapien
4	216	14.0	425	4 016042	016042 homo sapien
5	212.5	13.8	417	11 0920W1	0920W1 mus musculu
6	211.5	13.8	260	11 099NE0	099NE0 mus musculu
7	205.5	13.4	433	11 0912M6	0912M6 rattus norv
8	204.5	13.3	401	13 09PRG7	09PRG7 xenopus lae
9	203.5	13.2	169	11 09JKE0	09JKE0 rattus norv
10	201.5	13.1	459	11 062327	062327 mus musculu
11	194.5	12.6	283	4 096J31	096J31 homo sapien
12	193.5	12.6	222	11 099NE1	099NE1 mus musculu
13	193.5	12.6	234	11 099NE2	099NE2 mus musculu
14	191.5	12.5	430	6 09N092	09N092 macaca fasc
15	190.5	12.4	283	6 09XS28	09XS28 cercopithec
16	188	12.2	482	11 088734	088734 mus musculu

17	182.5	11.9	430	4 096924	096924 homo sapien
18	181.5	11.8	203	4 09BYU0	09BYU0 homo sapien
19	181.5	11.8	430	4 096J01	096J01 homo sapien
20	178	11.6	387	13 09PYD4	09PYD4 xenopus lae
21	174	11.3	401	4 000300	000300 homo sapien
22	173	11.2	203	11 099NE3	099NE3 mus musculu
23	171	11.1	327	11 09DC01	09DC01 mus musculu
24	171	11.1	461	11 091Y93	091Y93 rattus norv
25	171	11.1	461	11 091V30	091V30 rattus norv
26	167.5	10.9	651	13 0985M6	0985M6 gallus gall
27	164.5	10.7	186	12 072735	072735 compox viru
28	162	10.5	186	12 09YBP7	09YBP7 compox viru
29	160.5	10.4	372	4 09UHP4	09UHP4 homo sapien
30	158.5	10.3	438	13 09DEVO	09DEVO brachydanio
31	157.5	10.2	186	12 09WJB4	09WJB4 vaccinia vi
32	157.5	10.2	655	11 09EPUS	09EPUS mus musculu
33	157.5	10.2	655	11 091XK9	091XK9 mus musculu
34	157.5	10.2	655	11 091W77	091W77 mus musculu
35	155.5	10.1	186	12 091IR5	091IR5 vaccinia vi
36	154	10.0	655	4 075509	075509 homo sapien
37	152.5	9.9	316	12 057092	057092 ectromelia
38	152	9.9	401	11 008727	008727 rattus norv
39	151.5	9.9	320	12 057300	057300 ectromelia
40	151.5	9.9	320	12 057091	057091 ectromelia
41	151	9.8	401	11 008712	008712 mus musculu
42	150.5	9.8	320	12 057079	057079 compox viru
43	149.5	9.7	349	12 089118	089118 variola vir
44	147.5	9.6	348	12 057277	057277 monkeypox v
45	147.5	9.6	348	12 057103	057103 monkeypox v

## ALIGNMENTS

RESULT 1  
ID 002764 PRELIMINARY: PRT: 267 AA.  
AC 002764:  
DT 01-JUL-1997 (TREMBLrel. 04, Created)  
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE 0X40 PRECURSOR (FRAGMENT).  
OS Oryctolagus cuniculus (Rabbit).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
OX NCBI\_Taxid=9986;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CHB:HM;  
RA Isono T., Seto A.;  
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines.";  
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AB003911; BAA20059.1; -;  
DR HSSP: P25942; 1CDF.  
DR InterPro: IPR001368; TNFR\_C6.  
DR Pfam: PF00020; TNFR\_C6; 3.  
DR ProDom: PD000771; TNFR\_C6; 1.  
DR SMART: SM00208; TNFR\_3;  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 2.  
DR PROSITE: PS00500; TNFR\_NGFR\_2; 2.  
KW Signal.  
FT SIGNAL.  
FT NON\_TER  
FT CHAIN  
SQ SEQUENCE 267 AA: 28489 MW; ABB4CD3173C9500B CRC64;

Query Match 60.1%; Score 924; DB 6; Length 267;  
Best Local Similarity 67.3%; Pred. No. 6.6e-77;  
Matches 177; Conservative 23; Mismatches 59; Indels 4; Gaps 2;  
QY 15 ALLILGLSTVTGLHCVDYTPSNDRCCHCRPGNGMVSRCSSQNTVCRCGPGFYND 74

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Db 9 ALLLGLLGAEPDPDGVDTYGGDRCCLEQPGYMWSCNRSODTICHPCEPGFYNE 68
Oy 75 VVSSKPCRCCTCNLRSGSERKOLCTATODTCRCRAGTODPLDPSYGVGACAPCPGHS 134
Db 69 AVNYQACRCKCTOCNRRSGSEPOECHTHTDTCRCRPGTQPLNGYHGVDCAPCPGHS 128
Oy 135 PGDNQACRPMNCTLAGKHTLQPASNSDAICEDRDPATOPQETGPPARPITVOPTEA 194
Db 129 EGNRRACRPMNCTLAGKRTLOPASSISDAVCEDRSSLATQWEPFSPARPTARTSTA 188
Oy 195 WRTSGPSTRVEYVGGAAVAAILGLVLGLPLALLLYLRQRLPRAHKRP 254
Db 189 WRTAGGPTPLLEASKGQALVLSLGLGLALLLALYLHQRMR--PP--KLP 244
Oy 255 GGSFPTPIOEQADAHSTLAKI 277
Db 245 GGSFPTPIOEQADAGSTMAKI 267

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RESULT 2
Q9DDD2 PRELIMINARY: PRT: 276 AA.
AC 09DDD2:
DT 01-MAR-2001 (TREMBlrel. 16, Created)
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE HUMAN CD40-HOMOLOGUE.
GN TNFSF5.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Tregeastes C.A.;
RL Thesis (2001). University of Reading, Reading, UNITED KINGDOM.
DR EMBL; AJ293700; CAC20218.1; -.
DR HSP; P25942; ICDF.
DR InterPro: IPR001005; MYD_DNA_bind.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 3.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 3.
SQ SEQUENCE 276 AA; 30009 MW; 4040B7E0DB82454E CRC64;

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Query Match 14.9%; Score 229.5; DB 13; Length 276;  
 Best Local Similarity 27.1%; Pred. No. 2,9e-13;  
 Matches 74; Conservative 25; Mismatches 97; Indels 77; Gaps 10;

```

Oy 7 RLRGRGCAALLLGLSLVTVGLHCVDYPRNDRCRCHRGNGVNSCSNSQNTVCRP 66
Db 3 RGLGLGLCALLLGCG-QPGDAVNSDKQYEHKRCNCNQGPKKIASCNTEDSVCTP 61
Oy 67 CGPGFY-NDVSSKPCCKPCTWNCNLSGSEKOLCTATODTCRCRAGTODPLDPS 118
Db 62 CENGGOYHSMWTEKHCRTPEICEDNAGLIVKRGNATHNTVQCGRGMHCSDASQCTVE 121
Oy 119 ---YKGV-----DCARCPGHS--PEDNQACRPMNCTLAGKHTLQPASN 160
Db 122 NBPCKGFGFVAAMEARMTSPCEPCAECTFSNVSKTEPCHEFTWSCHEKGLVVKVGTN 181
Oy 161 SSDAICEDDP-----PATQPEF-----OGP-----PARPTV 189
Db 182 TSDVCESSRRSSLSYLITTAAYTCLVGICTYCVHTDLRRRGKQAEAPRELVTQ 241
Oy 150 OPTAMPRTSGPSTRVEP-----GGRAYA 216
Db 242 QPFE-----VDFPVQETLLGGQPYA 261

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RESULT 3
O95407 PRELIMINARY: PRT: 300 AA.
AC 095407:
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE DECOY RECEPTOR 3 (M68) (M68C) (DU583p15.1.1) (TUMOR NECROSIS
DE FACTOR RECEPTOR SUPERFAMILY, MEMBER 6B, DECOY).
GN DCR3 OR TR6 OR TNFRSF6B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE-99087326; Pubmed-9872321;
RA Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Mood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Borstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RA TISSUE-BLOOD:
RC MEDLINE-99253915; Pubmed-10318773;
RX "u.k.y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE-PANCREAS;
RX Bai C., Connolly B., Metzger M.L., Hillard C.A., Liu X., Sandig V.,
RX Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;
RT "Overexpression of M68/DCR3 in human gastrointestinal tract tumors
RT independent of gene amplification and its location in a four-gene
RT cluster.";
RL Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).
RN [4]
RP SEQUENCE FROM N.A.
RA Matthews L.;
RL Submitted (NOV-2000) to the EMBL/Genbank/DBJ databases.
RN [5]
RP SEQUENCE FROM N.A.
RC TISSUE-LUNG CARCINOMA, LARGE CELL UNDIFFERENTIATED.;
RA Strausberg R.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF104419; AAD03056.1; -.
DR EMBL; AF134240; AAD29688.1; -.
DR EMBL; AF217796; AAF35244.1; -.
DR EMBL; AF217793; AAF33685.1; -.
DR EMBL; AF217794; AAF33686.1; -.
DR EMBL; AL121845; CAC03668.1; -.
DR EMBL; BC017065; AAH17065.1; -.
DR HSP; O14763; 1D0G.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNFR_C6.
DR Pfam: PF00020; TNFR_C6; 4.
DR ProDom: PD000771; TNFR_C6; 1.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
SQ SEQUENCE 300 AA; 32679 MW; F90AE833718449AF CRC64;

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Query Match 14.7%; Score 226; DB 4; Length 300;
Best Local Similarity 27.0%; Pred. No. 6.5e-13;
Matches 80; Conservative 25; Mismatches 117; Indels 74; Gaps 12;

Qy 11 GPCALLLLGLGLSTVTLACY-----GDTYPSNDR-----CCHCRPGNGMVRCSRS 59
Db 6 GPGSLTCLVTLALPALLPVAVRGVAETPTYPWMDAETGERLYVCAQCPCPTGFVQRRCRD 65

Qy 60 QNTVCRPCGPGFYNDVSVSKCKPCTMCNLRSQ--SEBKOLCTATQDVTVCRCRAG----- 112
Db 66 SPTTCGCPPPPHNYTGFWMY--LERCRVCNVLCGEREEBARRCHATHNACRCRCTFFFAHA 123

Qy 113 --TOPLDSYKPG-----VDCAPCPGHP--SPGDNQACKPWTNCTLAKHTLQ 156
Db 124 GFCLEHASCPPGAGVIARTGPSQNTQCCPCPGTFSASSSSSEQCPRHNCALSLALNV 183

Qy 157 PASNSSDAICEDRDPATQPOETGCPARP-----TWQPRE 193
Db 184 PGSSSHDPLCTS--CTGFPPLSTRVPGAECEERAVIDEVAFODISIKRLQRLQALFAPE 240

Qy 194 AMPRTSGPSTRVEVPGGRAVAATLGLVIGLGPL--HIALALYLRRDRLP 247
Db 241 GW-----GPTPR-----AGRAALQKLRRRLTELLGADGALLVRLQALRVARRP 286

RESULT 4
ID 016042 PRELIMINARY; PRT; 425 AA.
AC 016042.
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DR 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE TUMOR NECROSIS FACTOR RECEPTOR (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCB1_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91370690; PubMed=1966549;
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
RA Brockhaus M., Lesslauer W.;
RT "Two human TNF receptors have similar extracellular, but distinct
RT intracellular, domain sequences.";
RL Cytochrome 2:231-237(1990).
DR EMBL: S63368; AAB19824.2; -.
DR HSSP: P25942; ICDF.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 4.
DR ProDom: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON_TER
SQ SEQUENCE 425 AA; 44608 MW; 1B24A97E3AD4CF9F CRC64;
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Qy 189 V--OPTAMPRTSGPSTR-----PVEVPGRAVAATLGLGLVGL--LGLPLAI 233
Db 186 TRSQHTQPTPEPSTRAPSTSFLLPMGPSPPAESSTGDFALPVGLIVATLGLITI 240

RESULT 5
ID 0920W1 PRELIMINARY; PRT; 417 AA.
AC 0920W1.
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DR 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE NERVE GROWTH FACTOR RECEPTOR.
CN NGRF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCB1_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A;
RX MEDLINE=99077793; PubMed=9857182;
RA Tuftereau C., Benejean J., Blondel D., Kieffer B., Flamaud A.;
RT "Low-affinity nerve-growth factor receptor (P75NTR) can serve as a
RT receptor for rabies virus.";
RL EMO J. 17:7250-7259(1998).
DR EMBL: AF105292; A011943.1; -.
DR HSSP: P07174; INGR.
DR MGD: MGI:97323; NGRF.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR000734; Lipase.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00531; Death_1.
DR Pfam: PF00020; TNFR_c6; 4.
DR SMART: SM00208; DEATH; 3.
DR PROSITE: PS50017; DEATH DOMAIN; 1.
DR PROSITE: PS01186; EGF_2; UNKNOWN_1.
DR PROSITE: PS00120; LIPASE_SER; UNKNOWN_1.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 4.
KW Receptor.
SQ SEQUENCE 417 AA; 44686 MW; 5D7A4510DB8AF9B2 CRC64;
```

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Query Match 13.8%; Score 212.5; DB 11; Length 417;
Best Local Similarity 30.2%; Pred. No. 1.6e-11;
Matches 78; Conservative 27; Mismatches 98; Indels 55; Gaps 14;

Qy 16 LLLDLGLSTVYGLH-CVGDYTPSNDRCCHCRPGNGMVRCSRSQNTVYCRPGCGF-YN 73
Db 9 LLLDLGLVSGFGAKETCSGMTYTHSGECCACNLGEGVAQPCGANQ-TVCEPCLDLSVTF 67

Qy 74 DVVS-SKPCPKCTWC-NLRSGSERKQLCTATQDVTVCRCRAGTQPLDSY----- 119
Db 68 DVVSATPECKPCTECLGLDLSMSAP---CYEADDAVCKRSGYGYQDEEFGRCACSGCYG 124

Qy 120 -----KPGVDACPCPPGHSPGDNA--CKPWTNCTLAKHTLQPASNSSDAICED 168
Db 125 SGLVSCQDKQNTVCECEGEGYTSDEANHVDCPLCTVCE-DTERQLRRECTWMADECE 183

Qy 169 -----RDP-----ATQP--QETQGPAPARTIVQPTAMPRTSGPSTRVE----- 208
Db 184 IPRMTRSTRPEGSDDVTTPSTOEPEAPERDL-IASIVADVTVTYMGSSQDPVVTRGTA 242

Qy 209 --VPGRAVAATLGLGLV 224
Db 243 NLIPYCSILAIVVGLV 260

RESULT 6
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099NE0
ID 099NE0 PRELIMINARY; PRT: 260 AA.
AC 099NE0;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE CD40 type V ISOFORM.
GN CD40.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=2111710; PubMed=11172023;
RA Tane M., Tane Y., Fairchild P.J., Wykes M., Waldmann H.;
RT "Regulation of CD40 function by its isoforms generated through
RT alternative splicing";
RL Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).
DR EMBL; AJ401390; CAC29430.1; -.
DR HSP; P25942; 1CDE.
DR InterPro: IPR001005; Myb_DNA_bind.
DR InterPro: IPR001865; Ribosomal_S2.
DR InterPro: IPR001368; TNR_C6.
DR Pfam; PF00020; TNR_C6; 4.
DR ProDom; PD000771; TNR_C6; 1.
DR SMART; SM00208; TNR; 4.
DR PROSITE; PS00037; MYB_1; UNKNOWN_1.
DR PROSITE; PS00962; RIBOSOMAL_S2_1; UNKNOWN_1.
DR PROSITE; PS00652; TNR_NGFR_1; 1.
DR PROSITE; PS00050; TNR_NGFR_2; 4.
SQ SEQUENCE 260 AA; 28895 MW; 57ASBACE8CF2F546 CRC64;

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Query Match 13.8%; Score 211.5; DB 11; Length 260;
Best Local Similarity 27.2%; Pred. No. 1.2e-11;
Matches 59; Conservative 27; Mismatches 68; Indels 63; Gaps 10;

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QY 26 VGLH-----CVGDTYPSNDRCHRCHECPGNGVSRCSQNTVCRPGCGFYNDVSSK 79
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 15 LVAHVGOCVTSKQYLDHGGCCDLCOPGSRILSHCTALEKTQCHPCDSGFSQAQMBE 74
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 80 -PCKPCTWGNLNGSERRKQLTATQDTQVCRAG----- 112
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 75 IRCHQHRHCEPNOGLRVKKEGTAEISDTVCTCKEGQHTSKDCBACQHPICPGFVMEH 134
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 113 -TOPLDYKPGVDCAPRGHSPGDNQA-----CKPWTNCTLAGKHTLQPASNSSDAIC 166
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 135 ATEETDTV-----CHPCPGFES---NQSLEFKCYPMWSCEDKNLEVLQKTSQINVIC 186
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 167 E-----DRD--PRATQ---DQETGPP---ARPI 187
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 187 EKVVKKRKNEMLRPAARQDDQEMEDYPGHNTAAIV 223
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 7
Q912M6 PRELIMINARY; PRT: 433 AA.
ID 0912M6;
AC 0912M6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR TYPE II (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p65 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport

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RT through the blood-brain barrier.";
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
KW Receptor.
FT NON_TER 1 1
FT NON_TER 433 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

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Query Match 13.4%; Score 205.5; DB 11; Length 433;
Best Local Similarity 26.8%; Pred. No. 7.2e-11;
Matches 68; Conservative 34; Mismatches 89; Indels 63; Gaps 13;

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QY 42 CCHCRPBGNGVSRCSRSQNTVCRPGCGFYNDVSSKPCPCPTWGNLNGSERRQL--C 99
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 34 CCAKCPBGYAKHFCMKTSPTVCADCAAGFQVMNH--LHTCLSSSSCSDDQVETMNC 91
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 100 TATQDTVCRGCRAGTQPLDSI-----KPG-----VCAAC 128
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 92 TKQNRVACANA-----DSYCALKLHSGNCRQCMKLSKCGPGVARSRTSNQNVICSAG 146
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 129 PCHFS--PGDNQACKPWTNCTLAGKHTLQPASNSSDAICEDRP--PATOPQETGPPAR 185
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 147 AEGTFSDTSSIDVCRPHRICSLA----IPGASIDAVCASPSIPSAVPRITVYQBE 202
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 186 PITVQPTAMPRTSGP-----STRPYE--VPGGRAVAAILGLVLGL--LGPLAIL 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 203 PTHSQMDDEPGSPQPHIPVLSGTPRIETPTGTS----LPGLIYGLTFLGLMLMG 258
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 235 LA-LYLRRDQRLP 247
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 259 LANCFTLVQRKKP 272
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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RESULT 8
Q9PRG7 PRELIMINARY; PRT: 401 AA.
ID 09PRG7;
AC 09PRG7;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE P75 NEUROTROPHIN RECEPTOR A-2.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipridae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Hutson L.D., Richards A.P., Bothwell M.;
RT "Life and death in the developing Xenopus retina: The role of the p75
RT neurotrophin receptor.";
RL Submitted (Jul-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF172400; AAD51031.1; -.
DR EMBL; AF172399; AAD51030.1; -.
DR HSP; P07174; INGR.
DR InterPro: IPR000488; Death.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR001368; TNR_C6.
DR Pfam; PF00531; death; 1.
DR Pfam; PF00020; TNR_C6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNR; 4.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00652; TNR_NGFR_1; UNKNOWN_3.
DR PROSITE; PS00050; TNR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 401 AA; 43419 MW; D13BCAF7863EFCF CRC64;

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Query Match 13.3%; Score 204.5; DB 13; Length 401;

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Best Local Similarity: 27.7%; Pred. No. 8.3e-11; Matches: 66; Conservativity: 28; Mismatches: 87; Indels: 57; Gaps: 13

[illegible]

Db	75	IRCHQHRRICELNQGLOVYKWKBBETAASDPIYVCTCKBEOHCAKNECEFCACGHRPCGFGFYVQM	134
Oy	113	-TQPLDSTKPGVDCAPCPGHFSFGDN--QACKWTNC	147
		I: I: I I I I I I I I I I I I I I I I	
Db	135	ATETDTIV-----CQCPVPGFSGSSSLFEKCHPWTC	167
RESULT	10		
ID	062327	PRELIMINARY:	PRT: 459 AA.
AC	062327;		
DT	01-NOV-1996	(TREMBLrel. 01, Created)	
DT	01-NOV-1996	(TREMBLrel. 01, Last sequence update)	
DT	01-DEC-2001	(TREMBLrel. 19, Last annotation update)	
DE	MURINE TUMOUR NECROSIS FACTOR RECEPTOR 2 PROTEIN (FRAGMENT).		
	MUS musculus (Mouse).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
OX	NCBI_TaxID=10090;		

RP		SEQUENCE FROM N.A.
RC		STRAIN=NOD;
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;	
RT	"Amino acid variation in the tumor Necrosis factor receptor 2 is linked to autoimmune diabetes in NOD mice.";	
RL	Genomics 0:0-0(0).	
RN	[2]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=NOD;	
RX	MEDLINE=95178848; PubMed=7873884;	
RA	Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;	
RT	"Allelic variation of the type 2 tumor necrosis factor receptor gene.";	
RL	Mamm. Genome 5:726-727(1994).	
DR	EMBL; X76401; CAAS3981.1; -. HSSP; P19438; INCF.	
DR	InterPro: IPR001368; TnFR_c6.	
DR	Pfam; PF000020; TnFR_c6; 4. Pfam; PF000071; TnFR_c6; 1.	
DR	ProDom; PD000771; TnFR_c6; 1.	
DR	SMART; SMO0208; TnFR; 4.	
DR	PROSITE; PS00652; TnFR_NGFR_1; 2.	
DR	PROSITE; PS50050; TnFR_NGFR_2; 3.	
KW	Receptor.	
FT	NON_TER	1
FT	VARIANT	87 1
FT	VARIANT	87 S -> T.
FT	VARIANT	93 T -> I.
FT	VARIANT	268 F -> I.
FT	VARIANT	345 S -> F.
FT	VARIANT	421 Y -> C.
SQ	SEQUENCE	459 AA; 46866 MW; 6C51D2FC1C4626DF CRC64;

[illegible]

DB 262 LGLVNCFLVORRKKKPSCLQDRAKVPHPD 291

RESULT 11  
096J31 PRELIMINARY: PRT: 283 AA.

AC 096J31;  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY, MEMBER 14 (HEPESVIRUS ENTRY MEDINTOR).  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxId=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=MELANOMA;  
RA Submitted R.;  
DR EMBL: BC002794; AA02794.1; --  
KW Receptor.  
SQ SEQUENCE 283 AA: 30420 MW: DFCEL46E4E024F4B CRC64:

Query Match 12.6%; Score 194.5; DB 4; Length 283;  
Best Local Similarity 28.8%; Pred. No. 4.7e-10;  
Matches 46; Conservative 14; Mismatches 59; Indels 41; Gaps 5;

QY 31 CVGDTPSNDRCHECRPGNGVNSCSRSQNTVCRPGGPFYNDVVS-KPKCKPTWNL 89  
DB 42 CDEDEPVCSECCPKSPGYRVKACGELTGVCPECPGTYIAHLNGLSKLCQCMCDP 101  
QY 90 RGSERKOLCTATODTVCRAG-----RAGTOPLDXY 119  
DB 102 AMGLRASRNCSTRTEVAVCCSPGHCTVODGDHCAACRAVYATSSPGQVQKGTESQDTL 161  
QY 120 KPGVDCAPCPGHFSP-GDNOACKPWTNC-----TLAKKHT 154  
DB 162 -----CONCPGTFSPNGLTECQHQTCSWLYTKAGACT 196

RESULT 12  
099NE1 PRELIMINARY: PRT: 222 AA.  
AC 099NE1;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CD40 TYPE IV ISOFORM.  
GN CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21117110; PubMed=11172023;  
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
RT "Regulation of CD40 function by its isoforms generated through alternative splicing."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
DR HSP: P25942; ICDP.  
DR InterPro: IPR001005; MYD\_DNA\_bind.  
DR InterPro: IPR001865; Ribosomal\_S2.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR\_4.  
DR PROSITE: PS00037; MYB\_1; UNKNOWN\_1.

DR PROSITE: PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE: PS00050; TNFR\_NGFR\_2; 4.  
SQ SEQUENCE 222 AA: 24499 MW: EF21E6C76FB42DEF CRC64:

Query Match 12.6%; Score 193.5; DB 11; Length 222;  
Best Local Similarity 26.7%; Pred. No. 4.5e-10;  
Matches 48; Conservative 23; Mismatches 62; Indels 47; Gaps 6;

QY 26 VVGLH-----CVGDTPSNDRCHECRPGNGVNSCSRSQNTVCRPGGPFYNDVVS 79  
DB 15 LTAIVHLGQCVTSCDKQYLHDGQCCDLCQGSRLTSHCTALEKTQCHPCDSGERSAQMRE 74  
QY 80 -PCKPTWNLRSERKOLCTATODTVCRAG----- 112  
DB 75 IRCHQHRHCEPNQGLRVKKEGTAEVDTCCKRGQHTSKDEACAGHTPCIPGFCVME 134  
QY 113 -TOPLDSTYKPGVDCAPCPGHFSPGDNQ-----CKPWTNCTLAGKHTLQPSNNSDAIC 166  
DB 135 ATETTDTV-----CHPCPVGFES---NQSLEPKCYPMTSCEDKNLEVLQKGTSTQTNVIC 186

RESULT 13  
099NE2 PRELIMINARY: PRT: 234 AA.

AC 099NE2;  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
DE CD40 TYPE III ISOFORM.  
GN CD40.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxId=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21117110; PubMed=11172023;  
RA Tone M., Tone Y., Fairchild P.J., Wykes M., Waldmann H.;  
RT "Regulation of CD40 function by its isoforms generated through alternative splicing."  
RT Proc. Natl. Acad. Sci. U.S.A. 98:1751-1756(2001).  
DR EMBL: AJ401388; CAC29428.1; --  
DR HSP: P25942; ICDP.  
DR InterPro: IPR001005; MYD\_DNA\_bind.  
DR InterPro: IPR001865; Ribosomal\_S2.  
DR InterPro: IPR001368; TNFR\_c6.  
DR Pfam: PF00020; TNFR\_c6; 4.  
DR ProDom: PD000771; TNFR\_c6; 1.  
DR SMART: SM00208; TNFR\_4.  
DR PROSITE: PS00037; MYB\_1; UNKNOWN\_1.  
DR PROSITE: PS00962; RIBOSOMAL\_S2\_1; UNKNOWN\_1.  
DR PROSITE: PS00652; TNFR\_NGFR\_1; 1.  
DR PROSITE: PS00050; TNFR\_NGFR\_2; 4.  
SQ SEQUENCE 234 AA: 25747 MW: 00DB1DD38347E325 CRC64:

Query Match 12.6%; Score 193.5; DB 11; Length 234;  
Best Local Similarity 26.7%; Pred. No. 4.8e-10;  
Matches 48; Conservative 23; Mismatches 62; Indels 47; Gaps 6;

QY 26 VVGLH-----CVGDTPSNDRCHECRPGNGVNSCSRSQNTVCRPGGPFYNDVVS 79  
DB 15 LTAIVHLGQCVTSCDKQYLHDGQCCDLCQGSRLTSHCTALEKTQCHPCDSGERSAQMRE 74  
QY 80 -PCKPTWNLRSERKOLCTATODTVCRAG----- 112  
DB 75 IRCHQHRHCEPNQGLRVKKEGTAEVDTCCKRGQHTSKDEACAGHTPCIPGFCVME 134  
QY 113 -TOPLDSTYKPGVDCAPCPGHFSPGDNQ-----CKPWTNCTLAGKHTLQPSNNSDAIC 166  
DB 135 ATETTDTV-----CHPCPVGFES---NQSLEPKCYPMTSCEDKNLEVLQKGTSTQTNVIC 186



RESULT 14  
 ID 09N092 PRELIMINARY: PRT: 430 AA.  
 AC 09N092: 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)  
 DE UNNAMED PROTEIN PRODUCT.  
 OS Macaca fascicularis (Crab eating macaque) (Cynomolgus monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Cercopitheciinae; Primates; Catarrhini; Cercopitheciidae;  
 OC Macaca  
 OX NCBI\_TaxID=9541;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Osada N., Hida M., Kusuda J., Tanuma R., Iseki K., Hirai M., Terao K.,  
 RA Suzuki Y., Sugano S., Hashimoto K.;  
 RT "Isolation of full-length cDNA clones from macaque brain cDNA  
 RT libraries."  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB046039; BAB01621.1;  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR SMART; SM00208; TNFR; 1.  
 SQ SEQUENCE 430 AA; 45850 MW; BA8DE92593E1E859 CRC64;

Query Match 12.5%; Score 191.5; DB 6; Length 430;  
 Best Local Similarity 28.2%; Pred. No. 1.4e-09;  
 Matches 78; Conservative 30; Mismatches 94; Indels 75; Gaps 14;

OY 16 ILLILGLSTVTLGLCVGDTYPSNDRCHCECRPGNGMVSRCSONTVCRPGCGFYNDY 75  
 DB 14 IMLLWPLATL-----STTLWQCPGE--EEDLNPGGSTLRCPCPGTFSSA 59  
 OY 76 VSSKPCPCCTWCLNLSGSRKQLCTATQDTVC-RCRAGTQPLDSYKP-GVDCAPCPGHE 133  
 DB 60 WSSSPQPHARCISLRLE-AQVGTAOTDLGDCWPGW----FGPMGVPRVPCQPCSM 113  
 OY 134 SPGDNACCKPMTNCTLAGKHTLQAPASNSSDAICEDRDPRATQPEQTGSPARITYQPT 193  
 DB 114 APLGIGHGCEWGRARRRGVEVAAGASSGE-----TRQP-- 147  
 OY 194 AMPRTSGQESTR---PVEVPGGRAVAAILGLIGLGLPLAILLALYLRDQRLPPDA 250  
 DB 148 -----GNGTRAGCEETRAQVAIAYIVPFCIMGLG-----ILVCNLKR-KGYHCTA 195  
 OY 251 HK---PPEGGS---FRPIQEQAADASHLAKI 277  
 DB 196 HKEVGPGGGGSGINPAYRT--EDVNEDTIGLVRL 230

RESULT 15

ID 09XS28 PRELIMINARY: PRT: 283 AA.

AC 09XS28: 01-NOV-1999 (TREMblrel. 12, Created)  
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HVEAS.  
 GN HVEAS.  
 OS Cercopithecus aethiops (Green monkey) (Grivet).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;  
 OC Cercopitheciinae; Cercopitheciidae;  
 OX NCBI\_TaxID=9534;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=KIDNEY;  
 RX MEDLINE=99296730; PubMed=10366573;  
 RA Foster T.P., Choulien V.N., Kousoulas K.G.;  
 RT "Functional characterization of the HveA homolog specified by African

RT green monkey kidney cells with a herpes simplex virus expressing the  
 RT green fluorescence protein."  
 RT Virology 258:365-374(1999).  
 DR EMBL; AF147720; AAD37381.1;  
 DR HSP; 014763; IDOG.  
 DR InterPro; IPR001368; TNFR\_C6.  
 DR Pfam; PF00020; TNFR\_C6; 3.  
 DR ProDom; PD000771; TNFR\_C6; 1.  
 DR SMART; SM00208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR\_1; UNKNOWN\_1.  
 DR PROSITE; PS50050; TNFR\_NGFR\_2; 2.  
 SQ SEQUENCE 283 AA; 30199 MW; 397951C6617FE3AA CRC64;

Query Match 12.4%; Score 190.5; DB 6; Length 283;  
 Best Local Similarity 26.3%; Pred. No. 1.1e-09;  
 Matches 66; Conservative 29; Mismatches 107; Indels 49; Gaps 12;

OY 12 PCAALLILGLSTVTLGLCVG-----DTPSNDRCHCECRPGNGMVSRCSONTV 63  
 DB 16 PKADITLVLYL-TFLGSSCYAPALPSCKEDEVPGSECCPKGPGFHVRAQCEGTGY 74  
 OY 64 CRPCGPGFY---NDVYSSKPCPCCTWCLNLSGSRKQLCTATQDTVCRCRAGTQPLDSY 119  
 DB 75 CEPCSPGTIYIAHENGSL---SKLQCCQCDPAMGLRTSRNCSITANALC----- 119  
 OY 120 KRGVDCAPCPGHE---SPGDN-QACKPMTNCTLAGKHTLQAPASNSSDAICEDRDPRATQ 175  
 DB 120 -----GSPGHFCITIQDHDHCAACRAYATSS-PQORVQGGTESQDTLQCN-CPGPT- 169  
 OY 176 PQTGPPAPRPITVQPTTEAMPRTSGQESTRPEVPGGRAVAAIL-GLIGLGLPLAIL 234  
 DB 170 -FSSNGTLEECQGNCKMKVLVTEAGPT-----SSSRWVWMLSSSLIYIVIGLIIR 223  
 OY 235 LALYLRDQR 245  
 DB 224 LITCVRRKRSR 234

Search completed: June 18, 2002, 14:26:16  
 Job time: 135 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:23:56 ; Search time 30.01 Seconds  
(Without alignments)  
1025.240 Million cell updates/sec

Title: US-09-852-845-2  
Perfect score: 1538  
Sequence: 1 MCVGARRLRGRCALLLLG.....SFRPIQEQDASHSLAKI 277

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues  
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: A.Geneseq\_032802.\*  
2: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1980.DAT.\*  
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16: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1994.DAT.\*  
17: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA1995.DAT.\*  
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22: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2000.DAT.\*  
23: /SIDSL/gcgdata/hold-geneseq/geneseq-emb1/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1538	100.0	277	16 AAR74737	ACT-4 cell surface
2	1538	100.0	277	16 AAR79904	ACT-4-n-1 receptor
3	1538	100.0	277	22 AAB53539	Human OX40 protein
4	1538	100.0	277	22 AAB50522	Human tumour necro
5	1496	97.3	277	16 AAR76996	Deduced sequence e
6	676.5	44.0	438	16 AAR81882	Plasmodium PDC406/OX4
7	676.5	44.0	438	16 AAR48976	OX40/FC mitein. C
8	676.5	44.0	205	22 AAB66985	OX40 protein. Uni
9	675.5	43.9	206	16 AAR81881	Mouse type-II memb
10	675.5	43.9	206	16 AAR48977	Mouse OX40 extrace
11	329	21.4	56	20 AAW94649	TNF-R extracellular

12	318	20.7	58	22	AAB69201	Human TNF-R extrac
13	248.5	16.2	415	22	AAB36700	Human tumour necro
14	247	16.1	451	19	AAW69951	RANK polypeptide p
15	247	16.1	451	19	AAW68287	RANK polypeptide p
16	247	16.1	451	22	AAE08732	Human receptor act
17	247	16.1	451	22	AAE04420	Human receptor act
18	247	16.1	451	22	AAE01987	Human 9D-15C clone
19	247	16.1	532	22	AAE02025	Human RANK deletio
20	247	16.1	544	22	AAE02024	Human RANK deletio
21	247	16.1	616	19	AAW69952	NF-kB receptor act
22	247	16.1	616	19	AAW68288	NF-kB receptor act
23	247	16.1	616	21	AAW53647	A human receptor a
24	247	16.1	616	22	AAE08733	Human receptor act
25	247	16.1	616	22	AAE04421	Human receptor act
26	247	16.1	616	22	AAE01988	Human full-length
27	247	16.1	616	22	AAW66560	Human RANK protein
28	246	16.0	622	22	AAE01999	Human FEO RANK (re
29	243.5	15.8	625	22	AAE02000	Human EP RANK (re
30	243	15.8	615	22	AAW30659	Human tumour necro
31	243	15.8	616	19	AAW79233	A receptor protein
32	236	15.3	591	19	AAW69950	RANK polypeptide p
33	236	15.3	591	19	AAW68286	RANK polypeptide p
34	236	15.3	591	22	AAE08731	Human receptor act
35	236	15.3	591	22	AAE04419	Human receptor act
36	236	15.3	591	22	AAE01986	Human 9D-8A clone
37	226	14.7	300	19	AAW66102	Amino acid sequenc
38	226	14.7	300	19	AAW63622	Human tumour necro
39	226	14.7	300	20	AAV03099	Human lung TNF-rec
40	226	14.7	300	20	AAV42182	Human FLINT #1 pro
41	226	14.7	300	20	AAV17479	Mammalian tumour n
42	226	14.7	300	20	AAV06817	Human DCR3 polypep
43	226	14.7	300	20	AAW97749	Human tumour necro
44	226	14.7	300	20	AAW95082	Orphan receptor (H
45	226	14.7	300	21	AAW19335	A full length huma

## ALIGNMENTS

RESULT 1	
AAAR74737	AAAR74737 standard; Protein: 277 AA.
XX	XX
AC	AAAR74737:
XX	XX
DT	21-NOV-1995 (first entry)
XX	XX
DE	ACT-4 cell surface receptor protein.
XX	XX
KW	Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system.
XX	XX
OS	Homo sapiens.
XX	XX
FH	Key
FT	Peptide
FT	/note= "signal peptide"
FT	Cleavage-site
FT	22..23 "signal cleavage site"
FT	Cleavage-site
FT	/note= "signal cleavage site"
FT	24..25 "signal cleavage site"
FT	Modified-site
FT	146..148
FT	/note= "glycosylation site"
FT	160..162
FT	/note= "glycosylation site"
FT	214..240
FT	/note= "transmembrane domain"
PN	WO9512673-A.
XX	XX
PD	11-MAY-1995.
XX	XX
PF	03-NOV-1994; 94NO-GB02415.
XX	XX

PR 03-NOV-1993: 93US-0147784.  
 XX  
 PA (BECT ) BECTON DICKINSON CO.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Buck DW, Engleman EG, Godfrey W;  
 XX  
 DR WPI: 1995-185777/24.  
 DR N-PSDB: AAQ88758.  
 XX  
 PT Isolated ACT-4 receptor from activated T-cells - also its ligands and  
 PT antibodies, useful for treating diseases of the immune system  
 XX  
 PS Claim 1: Fig. 5; 82pp; English.  
 XX  
 CC This sequence encodes the full-length cell surface receptor ACT-4  
 CC isolated from activated CD4+ T-lymphocytes. The sequence may be  
 CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or  
 CC fragments, and antibodies may be used for the treatment of transplant  
 CC rejection, graft-versus-host disease, autoimmune disease, etc.  
 XX  
 SQ Sequence 277 AA;

Query Match 100.0%; Score 1538; DB 16; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRPCAAALLLGLSTVTGTHCVGDTYPSNDRCHCRPGNGVSRCSRSO 60  
 DB 1 mcvgarrrlgrpcaa111lg1glstvtgthcvgdtypsndrchecrpgngvsrcrsq 60  
 OY 61 NTVCRRPGGFGFYNDVSSKPKPCCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120  
 DB 61 ntvcrrpggfyndvsskpkpcctwcnlrsgserkqlctatqdtvcrcragtqpldsyk 120  
 OY 121 PGVDCAPCPGPHFSFGDNQACKPWTNCTLAGKHTLQPA NSSDAICEPDRPATQPOETQ 180  
 DB 121 pgvdcapcpghfispgdackpwtnc1agkhtlqpasnsdaicedrppatqpetq 180  
 OY 181 GPAPRPITVQPTPEAMPRTSOGSPTRVPEVPGRAVAAILGLGLVGLPLAILLALYL 240  
 DB 181 gpaprpitvqptpeamprtsogsptrvpevpgravaailglglvlgllplail1a1yl 240  
 OY 241 RRDQRLPPDAHKKPGGSGFRTPIOEQADAHSTLAKI 277  
 DB 241 rrdqrlppdahkppgsgfrtpioeqadahstlaki 277

## RESULT 2

AAR79904 AAR79904 standard; Protein: 277 AA.

AC AAR79904;  
 DT 05-MAR-1996 (first entry)  
 XX  
 DE ACT-4-h-1 receptor sequence.  
 XX  
 KW ACT-4: specific binding partner: sbd; B cells; lymphocyte; GVHD;  
 KW graft versus host disease; immune response; transplantation;  
 KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;  
 KW HTLV; human T lymphocyte virus; inflammatory bowel disease;  
 KW screening; identification.  
 XX  
 OS Homo sapiens.

XX Key Location/Qualifiers  
 FH Cleavage-site 22..23  
 FT Cleavage-site /note= "Possible cleavage site."  
 FT Cleavage-site 24..25  
 FT Cleavage-site /note= "Possible cleavage site."  
 FT Modified-site 136..138

FT Modified-site 150..152  
 FT /label- glycosylation site.  
 FT Domain 204..230  
 FT /label- Transmembrane domain.  
 XX  
 XX W09521915-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 XX  
 PF 06-FEB-1995: 95MO-GB00238.  
 XX  
 XX  
 PR 10-FEB-1994: 94US-0195967.  
 XX  
 PA (GREAVES C P.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Engleman EG, Godfrey W;  
 XX  
 DR WPI: 1995-293117/38.  
 DR N-PSDB: AAT04048.

XX Ligand, ACT-4-L, to receptor on activated CD4 positive cells -  
 PT useful in treatment of various immune diseases and conditions  
 XX  
 PS Disclosure: Figure 5; 124pp; English.

CC ACT-4-L-h-1 is a specific binding partner (sbp) to the ACT-4  
 CC receptor polypeptide (encoded by this sequence) on the surface of  
 CC activated CD4 positive B cells. The sbp and its fragments are useful  
 CC in pharmaceutical applications to modify a patient's immune response  
 CC as well as having application in the treatment of transplant  
 CC rejection, graft versus host disease, autoimmune disease,  
 CC inflammation, infectious agents, HTLV infected cells or HIV.  
 CC Specifically, the sbd can be used to treat inflammatory bowel  
 CC disease. The sbd can also be used for screening for immunomodulatory  
 CC agents able to recognise ACT-4 and for monitoring activated CD4  
 CC positive cells or inhibiting infection of CD4 positive cells.  
 XX  
 SQ Sequence 277 AA;

Query Match 100.0%; Score 1538; DB 16; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRPCAAALLLGLSTVTGTHCVGDTYPSNDRCHCRPGNGVSRCSRSO 60  
 DB 1 mcvgarrrlgrpcaa111lg1glstvtgthcvgdtypsndrchecrpgngvsrcrsq 60  
 OY 61 NTVCRRPGGFGFYNDVSSKPKPCCTWCNLRSGSERKQLCTATQDTVCRCRAGTQPLDSYK 120  
 DB 61 ntvcrrpggfyndvsskpkpcctwcnlrsgserkqlctatqdtvcrcragtqpldsyk 120  
 OY 121 PGVDCAPCPGPHFSFGDNQACKPWTNCTLAGKHTLQPA NSSDAICEPDRPATQPOETQ 180  
 DB 121 pgvdcapcpghfispgdackpwtnc1agkhtlqpasnsdaicedrppatqpetq 180  
 OY 181 GPAPRPITVQPTPEAMPRTSOGSPTRVPEVPGRAVAAILGLGLVGLPLAILLALYL 240  
 DB 181 gpaprpitvqptpeamprtsogsptrvpevpgravaailglglvlgllplail1a1yl 240  
 OY 241 RRDQRLPPDAHKKPGGSGFRTPIOEQADAHSTLAKI 277  
 DB 241 rrdqrlppdahkppgsgfrtpioeqadahstlaki 277

## RESULT 3

AAB35329 AAB35329 standard; Protein: 277 AA.

XX  
 AC AAB35329;  
 XX

DT 08-MAY-2001 (first entry)  
XX  
DE Human OX40 protein SEQ ID NO: 3.  
XX  
KW Human: tumour necrosis factor receptor; TR13; TR14; infection;  
KW cancer; autoimmune disease; allergy; inflammatory disease;  
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.  
XX  
OS Homo sapiens.  
XX  
PN MO200105834-A1.  
XX  
PD 25-JAN-2001.  
XX  
PE 14-JUL-2000; 2000WO-US19343.  
XX  
PR 16-JUL-1999; 99US-0144087.  
PR 18-AUG-1999; 99US-0149450.  
PR 20-AUG-1999; 99US-0149712.  
PR 10-SEP-1999; 99US-0153089.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Ni J, Young PE.  
XX  
DR WPI; 2001-112682/12.  
XX  
XX Nucleic acids encoding 2 human tumor necrosis factor receptor  
PT polypeptides ((TR13) and (TR14)), useful for the prevention, diagnosis  
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and  
PT hypohidrotic ectodermal dysplasia -  
PS Disclosure; Page 372-373; 418pp; English.  
XX  
XX The present invention provides the protein and coding sequences of the  
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are  
CC useful in the diagnosis and treatment of many diseases, including cancer,  
CC autoimmune diseases, cardiovascular disorders, allergies,  
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and  
CC infections.  
XX  
SQ Sequence 277 AA:  
  
Query Match 100.0%; Score 1538; DB 22; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCVGARRLGRGPCAALLLGLSTVTGHLHCYGDTPPSNDRCHCPCPGNGVSRCSRSQ 60  
DB 1 mcvgarrrlgrgpcaalllllgstvtg hlcvgdtpsndrc hccpcpgngvsrcrsq 60  
QY 61 NTVCRCGPGFNDVSSPKPCPTWCNLRSSGSRKQLCTAODYVCRAGTGPLDSYK 120  
DB 61 ntvcrcpgpfndvsspkpcptwc nlrssgsrkqlctaod yvcragtpgldsyk 120  
QY 121 PGVDCAPCPGPHFSPGDNQACKPMTNCTLAGKHTLQPSNSSDAICEDRDPATPOETO 180  
DB 121 pgvdcapcpghfspgdnqackp mtntctlagkhtlq psnssdaicedr dpapatpoeto 180  
QY 181 GPPAPRTVQPEANPRTSOGSPTRPEVPGGRAVAAILIGLGLVGLGLPAILALTYL 240  
DB 181 gppaprtvqp eanp rtsogsptrpe vpggravaaili glglv glglpailal tyll 240  
QY 241 REDORLPPDAHKPPGSGSFRFPJOEODAHSTLAKI 277  
DB 241 rrdqrlppdahkppgsgsfrfpj oeodahstl aki 277

AC AAB50522;  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor OX40 protein SEQ ID NO:12.  
XX  
KW Human: tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neutrotropic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotrophic;  
KW immunosuppressive; neutrotrophic; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.  
XX  
OS Homo sapiens.  
XX  
PN MO200071150-A1.  
XX  
PD 30-NOV-2000.  
XX  
PE 18-MAY-2000; 2000WO-US13515.  
XX  
PR 20-MAY-1999; 99US-0135164.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Wei Y, Ruben SM, Gentz RL, Ni J;  
XX  
DR WPI; 2001-041051/05.  
XX  
XX Nucleic acid encoding a TR1D polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection -  
PS Disclosure; Fig 2: 285pp; English.  
XX  
XX The present invention describes the human TR1D protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor  
CC receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,  
CC neutrotropic, neutrotrophic, antiviral, antiinflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotrophic  
CC activities, and can be used in gene therapy. The TR1D polynucleotides  
CC are useful for detecting complementary polynucleotides. TR1D proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain hematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TR1D by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TR1D  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
CC (b) autoimmune disorders; (c) diseases associated with increased  
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The  
CC present sequence represents a tumour necrosis factor receptor used in  
CC comparison with TR1D in the exemplification of the present invention.  
XX  
SQ Sequence 277 AA:  
  
Query Match 100.0%; Score 1538; DB 22; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.2e-100;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCVGARRLGRGPCAALLLGLSTVTGHLHCYGDTPPSNDRCHCPCPGNGVSRCSRSQ 60  
DB 1 mcvgarrrlgrgpcaalllllgstvtg hlcvgdtpsndrc hccpcpgngvsrcrsq 60  
QY 61 NTVCRCGPGFNDVSSPKPCPTWCNLRSSGSRKQLCTAODYVCRAGTGPLDSYK 120  
DB 61 ntvcrcpgpfndvsspkpcptwc nlrssgsrkqlctaod yvcragtpgldsyk 120

```

Db      61 ntvcrcpgpgfyndvsvskpckpctwcnlrsgerqkqlctatqdtvcrcragtqpldsyk 120
Oy      121 PGVDCAPCPPGHFSPGDNOACKPWTNCTLAGKHTTLPASNSSDAICEDRDPATQPQEQ 180
        |||
Db      121 pyvdcapcppghfspdngackpwtctclagkhtlqpaanssdaicedrdpattqpcq 180
Oy      181 GPPARPIVQPTPEAWPRTSGPSTRPEVPGGRAVAAILGLIVGLPLAILLALYLL 240
        |||
Db      181 gpparpilvqptpawprtsqgsptrevpggravaailglivglplailallalyll 240
Oy      241 RRDQRLPPDAHKPPGGGSFRTPIQEOADAHSTLAKI 277
        |||
Db      241 rrdqrlppdahkppgggsftrtpiqeeqadahnstlaki 277

RESULT 5
AAR76996
ID      AAR76996 standard; Protein; 277 AA.
XX
AC      AAR76996;
XX
DT      21-DEC-1995 (first entry)
XX
DE      Deduced sequence encoded by human OX-40 cDNA.
XX
KW      Human OX-40; activated T-cells; CD4+ T-cells; antigen;
KW      multiple sclerosis; sarcoidosis; rheumatoid arthritis; uveitis;
KW      T-cell lymphoma.
XX
OS      Homo sapiens.
XX
PN      WO951251-A.
XX
PD      10-AUG-1995.
XX
PF      06-FEB-1995; 95WO-GB00237.
XX
PR      04-FEB-1994; 94US-0192480.
XX
PA      (WEIN/) WEINBERG A D.
PA      (CANT-) CANTAB PHARM RES LTD.
XX
PI      Vandenbark AA, Weinberg AD;
XX
DR      WPI: 1995-283771/37.
DR      N-PSDB: AA093257.
XX
PT      Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
PT      develop prods. for detection and therapy of conditions mediated by
PT      activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
XX
PS      Claim 3; Fig 11; 91pp; English.
XX
CC      Antigen OX-40 is specifically expressed on the cell surface of
CC      antigen activated T-cells, especially, for example, CD4+ T-cells. A
CC      human cDNA encoding the human OX-40 homologue was cloned as follows.
CC      Using the Experimental Autoimmune Encephalomyelitis model in rats
CC      the OX-40 antigen was identified (expressed on the surface of
CC      activated autogenous-specific CD4+ T-cells present at the site of
CC      inflammation but absent on CD4+ T-cells at non-inflammatory sites)
CC      and cDNA encoding the antigen was isolated. PCR primers were
CC      designed and used to clone murine OX-40 cDNA by PCR from RNA
CC      isolated from murine CD4+ T-cells activated with concanavalin A.
CC      Then the murine OX-40 cDNA was used to probe a cDNA lambda gtl1
CC      library from human activated T lymphocytes to obtain human OX-40
CC      cDNA. The published patent application states that the OX-40 cDNA
CC      sequence is also in SQ ID no. 1, but this sequence is not present
CC      in the spec. A nucleic acid having the sequence in SQ ID no 1 and
CC      the polypeptide encoded by it are claimed.
XX
SQ      Sequence 277 AA:

```

```

Query Match      97.3%; Score 1496; DB 16; Length 277;
Best Local Similarity 97.5%; Pred. No. 1, 1e-97;
Matches 269; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Oy      1 MCVGARLRGRCPCALLLLGLISTYTGILHCYVDTRYPSNDRCHEGRPNGMWSRCSRSQ 60
        |||
Db      1 mcvgarlrgrcpaallllglistvtglhcyvgdtrcpsndrcchegrpnmwsrscrsq 60
Oy      61 NTVCRCPGPGFYNDVSVSKPCKPCTWCNLRSGSERQQLTATQDTVCRCRAGTQPLDSYK 120
        |||
Db      61 ntvcrcpgpgfyndvsvskpckpctwcnlrsgerqkqlctatqdtvcrcragtqpldsyk 120
Oy      121 PGVDCAPCPPGHFSPGDNOACKPWTNCTLAGKHTTLPASNSSDAICEDRDPATQPQEQ 180
        |||
Db      121 pyvdcapcppghfspdngackpwtctclagkhtlqpaanssdaicedrdpattqpcq 180
Oy      181 GPPARPIVQPTPEAWPRTSGPSTRPEVPGGRAVAAILGLIVGLPLAILLALYLL 240
        |||
Db      181 gpparpilvqptpawprtsqgsptrevpggravaailglivglplailallalyll 240
Oy      241 RRDQRLPPDAHKPPGGGSFRTPIQEOADAHSTLAK 276
        |||
Db      241 rrdqrlppdahkppgggsftrtpiqeeqadahnstlvk 276

RESULT 6
AAR81882
ID      AAR81882 standard; Protein; 438 AA.
XX
AC      AAR81882;
XX
DT      30-MAR-1996 (first entry)
XX
DE      Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
XX
KW      OX40; OX40-L; cytokine; cell surface molecule; plasmid;
KW      pDC406/OX40/Fc*; membrane glycoprotein.
XX
OS      Synthetic.
XX
PN      US5457035-A.
XX
PD      10-OCT-1995.
XX
PF      23-JUL-1993; 93US-0097827.
XX
PR      23-JUL-1993; 93US-0097827.
XX
PA      (IMMV ) IMMUNEX CORP.
XX
PI      Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
DR      WPI: 1995-357992/46.
DR      N-PSDB: AAT00829.
XX
PT      New isolated DNA encoding the OX40 ligand polypeptide - also vectors
PT      and host cells, used to produce recombinant ligand used in e.g.
PT      prim. T cell culture, to modulate immune response etc.
XX
PS      Example 2; Column 35-38; 26pp; English.
XX
CC      This plasmid encodes an OX40/Fc antibody fragment mutein protein,
CC      and is used to express a soluble OX40/Fc mutein fusion protein for
CC      use in detecting cDNA clones encoding a OX40 ligand. The Fc
CC      fragment may be derived from human IgG1, and the plasmid may be
CC      used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell
CC      line. Culture supernatant was purified by affinity chromatography
CC      and this was used, together with labeled goat anti-human IgG to
CC      screen various cell lines.
XX
SQ      Sequence 438 AA:

```



XX Disclosure: Fig 2; 316pp; English.  
PS  
XX  
CC The present invention relates to a method for treating conditions leading  
CC to bone loss. The method comprises administering a purified and isolated  
CC osteoprotegerin (OPG) protein (AA057836-AA057838 and AA066974-AA066976)  
CC in conjunction with other substances such as tumour necrosis factor- $\alpha$  (TNF- $\alpha$ ) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet  
CC activating factor (PAF) antagonists. The method is useful for treating  
CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
CC graft-versus-host disease (GVHD). Other diseases that can be treated  
CC include acute pancreatitis, Alzheimer's disease, anorexia,  
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperaesthesia,  
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
CC psoriasis and septic shock. The present sequence was used in a sequence  
CC homology comparison.  
XX  
SQ Sequence 205 AA:

Query Match 44.0%; Score 676; DB 22; Length 205;  
Best Local Similarity 64.1%; Pred. No. 3,5e-40;  
Matches 123; Conservative 14; Mismatches 53; Indels 2; Gaps 1;  
OY 15 ALLLLGLSLTYTGLHCVDTPPSNDRCHCRPGNGVSRCSQNTVCRPGGFGYND 74  
DB 10 ALLLLGLSLTYTGLHCVDTPPSNDRCHCRPGGFGYND 69  
OY 75 VVSSKPKPCRTWCNLRSGSERKOLCTATODTYCRGACGTP--DSYKGVDCAPCPG 132  
DB 70 AVNYLTKYCTQCNLRSGSERKOLCTATODTYCRGACGTP--DSYKGVDCAPCPG 129  
OY 133 FSPGDNQACKPWTNCTLAGKHTLQPASNSDAICEDRDPPTQPOETGPPARPITYOP 192  
DB 130 FSPGDNQACKPWTNCTLAGKHTLQPASNSDAICEDRDPPTQPOETGPPARPITYOP 189  
OY 193 EAMPTSGCPST 204  
DB 190 LTVPTSGPST 201

RESULT 9  
AAR81881  
ID AAR81881 standard; Protein: 206 AA.  
XX  
AC AAR81881;  
XX  
DT 08-JUL-1996 (first entry)  
XX  
DE Mouse type-II membrane polypeptide OX40 extracellular domain.  
XX  
KW OX40: OX40-L: cytokine; cell surface molecule;  
XX  
KW membrane glycoprotein.  
XX  
OS Mus musculus.  
XX  
PN US5457035-A.  
XX  
PD 10-OCT-1995.  
XX  
PE 23-JUL-1993; 93US-0097827.  
XX  
PR 23-JUL-1993; 93US-0097827.  
XX  
RA (IMMUNEX ) IMMUNEX CORP.  
XX  
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
XX  
DR WPI: 1995-357992/46.

DR N-PSDB: AAT00826.  
XX  
XX  
PT New isolated DNA encoding the OX40 ligand polypeptide - also vectors  
PT and host cells, used to produce recombinant ligand used in e.g.  
PT prim. T cell culture, to modulate immune response etc.  
XX  
PS Example 1; Column 33-34; 26pp; English.  
XX  
CC This sequence encodes the extracellular domain of OX40, a membrane  
CC glycoprotein present on the CD4 positive subset of activated T  
CC cells.  
XX  
SQ Sequence 206 AA:

Query Match 43.9%; Score 675.5; DB 16; Length 206;  
Best Local Similarity 64.8%; Pred. No. 3,8e-40;  
Matches 125; Conservative 16; Mismatches 49; Indels 3; Gaps 2;  
OY 15 ALLLLGLSLTYTGLHCVDTPPSNDRCHCRPGNGVSRCSQNTVCRPGGFGYND 73  
DB 10 ALLLLGLSLTYTGLHCVDTPPSNDRCHCRPGGFGYND 69  
OY 74 DVVSSKPKPCRTWCNLRSGSERKOLCTATODTYCRGACGTP--DSYKGVDCAPCPG 131  
DB 70 AVNYLTKYCTQCNLRSGSERKOLCTATODTYCRGACGTP--DSYKGVDCAPCPG 129  
OY 132 HSPGDNQACKPWTNCTLAGKHTLQPASNSDAICEDRDPPTQPOETGPPARPITYOP 191  
DB 130 HSPGDNQACKPWTNCTLAGKHTLQPASNSDAICEDRDPPTQPOETGPPARPITYOP 189  
OY 192 TEAMPTSGCPST 204  
DB 190 LTVPTSGPST 202

RESULT 10  
AAW48977  
ID AAW48977 standard; Protein: 206 AA.  
XX  
AC AAW48977;  
XX  
DT 25-SEP-1998 (first entry)  
XX  
DE Mouse OX40 extracellular domain.  
XX  
KW OX40: cytokine; T cell antigen; TH-2 immune response; OX40-L;  
XX  
KW OX40/FC.  
XX  
OS Mus sp.  
XX  
PN US5783665-A.  
XX  
PD 21-JUL-1998.  
XX  
PE 22-JUN-1995; 95US-0494574.  
XX  
PR 23-JUL-1993; 93US-0097827.  
XX  
PR 22-JUN-1995; 95US-0494574.  
XX  
PA (IMMUNEX ) IMMUNEX CORP.  
XX  
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
XX  
DR WPI: 1998-427099/36.  
XX  
DR N-PSDB: AAV32640.  
XX  
PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell  
XX production and binding assays for OX-40 and homologues  
XX  
PS Example 1; Col 33-34; 26pp; English.  
XX  
CC The present sequence represents the mouse OX40 extracellular domain





CC related activation-induced cytokine (TRANCE)/receptor activator of  
 CC NF-kappa ligand (RANK) inhibitors. The method is useful for treating  
 CC diseases characterised by bone loss such as osteoporosis, Paget's  
 CC disease, metastatic bone disease, rheumatoid arthritis or periodontal  
 CC disease, and modulating dendritic cell maturation, T cell proliferation,  
 CC and/or CD40 receptor systems. The present sequence represents an  
 CC extracellular Cys-rich domain of a tumour necrosis factor receptor of  
 CC (TNF-R) superfamily member, which is used in the exemplification of  
 CC the present invention.

CC Sequence 58 AA:

Query Match 20.7%; Score 318; DB 22; Length 58;  
 Best Local Similarity 96.6%; Pred. No. 1.4e-15;  
 Matches 56; Conservative 0; Mismatches 0; Indels 2; Gaps 1;

QY 64 CRPGCGFNDVSSKPKRCQTCMNLRSSEKQOLCTATQ--DTVCRGAGTQPLDSY 119  
 DB 1 crpcgpgfndvsskpkrcqtcwcnlrsgserktqlctatqdcvtccrctagtpldsy 58

RESULT 13  
 AAB36700

ID AAB36700 standard; Protein; 415 AA.

AC AAB36700;

DT 15-MAR-2001 (first entry)

DE Human tumour necrosis factor receptor LTRB protein SEQ ID NO:6.

XX Human; tumour necrosis factor receptor 5; TRID; TNFR-5; TR5; noctropic;  
 KM TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
 KM tumour necrosis factor related apoptosis inducing ligand; vasotrophic;  
 KM immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
 KM anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
 KM gene therapy; restenosis; graft versus host disease; tumour; cancer;  
 KM apoptotic cell death related disease; autoimmune disorder;  
 KM cardiovascular disorder; viral infection.

XX Homo sapiens.

PN WO200071150-A1.

XX 30-NOV-2000.

XX 18-MAY-2000; 2000WO-US13515.

XX 20-MAY-1999; 99US-0135164.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Wei Y, Ruben SM, Gentz RL, NI J;

XX WPI; 2001-041051/05.

XX Nucleic acid encoding a TRID polypeptide, also referred to as tumor  
 PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
 PT prevention of cancer, autoimmune disorders and viral infection -

XX Disclosure: Fig 2; 285pp; English.

XX The present invention describes the human TRID protein (tumour necrosis  
 CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
 CC intracellular domain, also referred to as tumour necrosis factor  
 CC receptor 5 (TNFR-5 or TR5)). TRID has cytostatic, immunosuppressive,  
 CC neurotropic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
 CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
 CC activities, and can be used in gene therapy. The TRID polynucleotides  
 CC are useful for detecting complementary polynucleotides. TRID proteins and  
 CC polynucleotides are useful in the treatment of tumours, resistance to  
 CC parasite, bacteria and viruses, restenosis and graft versus host disease.

CC They are also useful for inducing proliferation of T-cells, endothelial  
 CC cells and certain haematopoietic cells, to regulate antiviral responses  
 CC and to prevent certain autoimmune diseases after stimulation of TRID by  
 CC an agonist or TRAIL binding facilitator. The antibodies which bind TRID  
 CC polypeptides are useful for treating and/or preventing diseases  
 CC associated with increased or decreased apoptotic cell death. The TRID  
 CC polynucleotides, proteins, antibodies, agonists and antagonists are  
 CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
 CC (b) autoimmune disorders; (c) diseases associated with increased  
 CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The  
 CC present sequence represents a tumour necrosis factor receptor used in  
 CC comparison with TRID in the exemplification of the present invention.

XX Sequence 415 AA:

Query Match 16.2%; Score 248.5; DB 22; Length 415;  
 Best Local Similarity 23.3%; Pred. No. 8e-10;  
 Matches 93; Conservative 39; Mismatches 126; Indels 141; Gaps 16;

QY 7 RLGR--GPCAL--LLGLGLSTVTGLHCVGDTY-----PSNDRCHE 45

DB 2 rlpaspcglawgpllllgslvaspgqlvpyrlentqtcwdqdkyepmhvccar 61

QY 46 CRPGCMVSRCSRSQNTVCRPCGPGFYNDVSS-KRCRCCTCMNLRSSEKQOLCTATQD 104

DB 62 cpggefivavcsrsqdtvctcphmsynehnhlctcqlcrpdlvlgfeevapctsdix 121

QY 105 TVCRCRAG-----TOPLDSYKPG-----VDCAPCPGHP--SP 135

DB 122 acrcqpgmscyldnechceerlvlcpgplaeavdeindtncvcpkphgnts 181

QY 136 GNOAQCPWNTCTLACKHTLQPASNSDAICEDRDPAT----- 174

DB 182 sprarcqbltceqlglveaagtsydticknppegamllla1191vllftvta 241

QY 175 -----QPQETQGP-----ARPI-----TQPTREAWPR 197

DB 242 cammrhpslcrklgllkthpegeesppepadphfdleplpmagdlspspasp 301

QY 198 TS-----QGPSTRPEV--PGRAVAAILGLG-VLGLGLPLAILLALVLR-- 241

DB 302 tapsleevlqgspdvqarelaeapgehgyahgansghvc--gsvctgulylyngp 359

QY 242 -----RDQRLPPDAHKP-----PGGGSFRTPIQEE 266

DB 360 vlgtrpgdpdpapepyrptpeegapgselstpyed 398

RESULT 14

XX AAM69951 standard; Protein; 451 AA.

XX AAM69951;

XX 08-OCT-1998 (first entry)

XX RANK polypeptide partial sequence encoded by cDNA clone 9D-15C.

XX RANK; necrosis factor-kappa B; NF-KB; receptor activator; human;

XX RANKL; RANK ligand; tumour necrosis factor; TNF.

XX Homo sapiens.

XX WO9828426-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23775.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059976.





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OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 2703.24 Seconds  
(without alignments)  
8190.274 Million cell updates/sec

Title: US-09-852-845-1  
Perfect score: 1058  
Sequence: 1 cagcagagcagcagatgtgc.....cacaataaacccttgcag 1058

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : GenBank:\*

1: gb\_pa:\*  
2: gb\_htg:\*  
3: gb\_in:\*  
4: gb\_om:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_sts:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
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25: em\_pl:\*  
26: em\_ro:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_htg\_hum:\*  
31: em\_htg\_inv:\*  
32: em\_htg\_other:\*  
33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
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1	1044.4	98.7	1057	6	AR048669	Sequence
2	1044.4	98.7	1057	6	AR156875	Sequence
3	1016.2	96.0	1034	9	S76792	OX40-cell s
4	888.2	84.0	1373	9	HSBOX40MR	
5	472.6	44.7	877	4	AB003911	Rabbit mr
6	389.8	36.8	111119	2	AL162741	Homo sapi
7	389.8	36.8	210944	2	AL390719	Homo sapi
8	388.2	36.7	5150	9	HSZ277151	Homo sapi
9	375.6	35.5	1017	10	RSOX40	X17037 Rat mRNA fo
10	373	35.3	883	10	MMOX40	
11	286.6	27.1	1317	6	AR019521	Sequence
12	286.6	27.1	1317	6	IL4936	Sequence 10
13	283.2	26.8	618	6	AR019518	Sequence
14	283.2	26.8	618	6	IL4933	Sequence 6
15	124.4	11.8	6080	6	AX251336	Sequence
16	111.2	10.5	117	6	AX134865	Sequence
17	111.2	10.5	117	6	AX134963	Sequence
18	111.2	10.5	117	6	AX135076	Sequence
19	109.4	10.3	117	6	AX134865	Sequence
20	109.4	10.3	117	6	AX134962	Sequence
21	109.4	10.3	117	6	AX135075	Sequence
22	108.8	10.3	6080	6	AX251335	Sequence
23	103.4	9.8	2907	10	MMDNROX40	
24	103.4	9.8	60953	2	AC1100470	Mus muscu
25	103.4	9.8	99098	2	AC095793	Rattus no
26	103.4	9.8	253111	2	AL627204	Mus muscu
27	103.4	9.8	254197	2	AF389853	Mus muscu
28	101.6	9.6	5148	6	AX251339	Sequence
29	79.8	7.5	5148	6	AX251340	Sequence
30	68.6	6.6	125020	9	AF429315	Homo sapi
31	68.2	6.5	125020	9	AF429315	Homo sapi
32	63.4	6.0	52359	2	AC010772	Homo sapi
33	62	5.9	197669	2	AC084064	Homo sapi
34	61	5.8	65869	2	AC090435	Chlamydom
35	61	5.8	100006	2	AC090436	Chlamydom
36	60.8	5.7	63629	2	AC091187	Homo sapi
37	59.2	5.6	303091	2	AC084799	Mus muscu
38	57	5.4	161307	2	AC084058	Homo sapi
39	56.8	5.4	113056	2	AC102988	Rattus no
40	56.2	5.3	224923	2	AC068947	Mus muscu
41	56	5.3	705	6	AF117297	Homo sapi
42	56	5.3	723	6	AX074382	Sequence
43	56	5.3	726	6	AF125304	Homo sapi
44	56	5.3	1006	6	AR108738	Sequence
45	56	5.3	1008	6	AX055408	Sequence

## ALIGNMENTS

RESULT 1.

LOCUS AR048669 1057 bp DNA linear PAT 29-SEP-1999

DEFINITION Sequence 1 from patent US 5821332.

ACCESSION AR048669

VERSION AR048669.1 GI:5971012

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

REFERENCE 1 (bases 1 to 1057)

AUTHORS Godfrey,W., Buck,D. and Engleman,E.G.

TITLE Receptor on the surface of activated CD4.sup.+ T-cells: ACT-4

JOURNAL Patent: US 5821332-A 1 13-0CT-1998;

FEATURES

source location/Qualifiers

BASE COUNT 176 a 390 c 344 g 147 t

ORIGIN

Query Match 98.7%; Score 1044.4; DB 6; Length 1057;  
Best local Similarity 99.8%; Pred. No. 1.1e-150;



D	b61	CCGCCATCCTGGGCTTGGGCGCTTGtGTGCTGGGGCTGTCTBGGCCCCCTGGCCATCCTGctgag	720
Oy	721	ccttgtaacctgtcctcggaaggacaaaggtctgcccccagatgaccacaagccccctggag	780
D	721	CCCTGTACTCTGCTCGGAGGAGACCAAGAGGCTGTCCCCTCATGTGCACAAAGCCCCCTGGGG	780
Oy	781	gagcagactttccgcgaaccccccaatccaagagggcagcggccgaagcccatcgaacctgacca	840
D	781	GAGGAGATTTCCTGGAGCCCAATCCAAAGGAGGAGGCGGAGGCGCCACCTCACCTGGGCA	840
Oy	841	agatctgacctgtgagcccaagaagtgaagctgtgagcccgcccaagctgtgagcccgagag	900
D	841	AGATCTGATC-TGGGCCCCAACGAAGTTGAGAGCTGGGCGCCGCCAAGCTGTGAGGCCGAGAG	899
Oy	901	gtctgtctggcgaagcagcagcaggtgtcaggtccgctgtcccgcccaagctctgtggccaact	960
D	900	GTCTGTCTGGGGAGAGGAGGCGAGGTGCAAGGCGCGCTGTGCCCCGCCACAGCTCTGGGGCCA	959
Oy	961	ctgcaacgttctaagtgtcgaattgtgtctgtccctcgagctcttccttaagatgatcatgata	1020
D	960	CTGCACCTTTCTAGTAGTGCCTGAGTGGCTGCTCGGCTCTCTGTCTTAAGATGATGCATGATA	1019
Oy	1021	cctctgccccgcggagaccacaataaaaaaacctgtgacg	1058
D	1020	CCTCCTGCCCGCGGAGACCACATMAAAACCTTGCGAG	1057
R	E	S/T6792	1034 bp mRNA linear PRI 02-JUN-2000
L	LOCUS	Ox40-cell surface antigen [human, mRNA partial, 1034 nt].	
D	DEFINITION	S/T6792	
V	VERSION	S/T6792.1 GI:913405	
K	KEYWORDS	human.	
S	SOURCE	Homo sapiens	
O	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
R	REFERENCE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
A	AUTHORS	1 (bases 1 to 1034)	
T	TITLE	Baum,P.R., Gayle,R.B.III., Ramsdell,F., Srinivasan,S., Grabsstein,K., Alderson,M.R. et.al.	
J	JOURNAL MEDLINE	Identification of Ox40 ligand and preliminary characterization of its activities on Ox40 receptor	
R	REMARK	Circ. Shock 44 (1), 30-34 (1994) 95219871	
F	FEATURES	Genbank staff at the National Library of Medicine created this entry [NCBI gidsbg 163567] from the original journal article.	
S	source	This sequence comes from Fig. 3A. Location/Dualifiers 1..1034 /organism="Homo sapiens" /db_xref="taxon:9606" <1..1034 /gene="Ox40" <1..825 /gene="Ox40" /note="cell surface antigen; This sequence comes from Fig. 3A" /codon_start=1 /product="Ox40" /protein_id="AAB33944.1" /db_xref="GI:913406" /translation="LARRLGRCPCALLLLGLSTVTGLHCWGDYTPSNDRCHCEPRPGNVAIRCSRSQNTVPCPGFYNVDVSSKPKPCTWCMLRSGSRKOLCTADTDTCVCRRAGQPLDYSKPGVDCAPCPGHSPEDNDACKPWITCKTLAGHTLTLPANSDDAICDDROPATPOQETGPPARPPIYTVOPTFAWPRTSGPSRPVEVGGRAVAIILGLIVGLIGLPAIILAITYLRDQRLPPAHNRPPGGSTRPIQEODAHSTLAKT"	
C	gene		
CDS			
B	BASE COUNT	169 a 386 c 333 g 146 t	
O	ORIGIN		

Query Match	96.0%	Score 1016.2	DB 9	Length 1034	
Best Local Similarity	99.6%	Pred. No. 2.4e-146			
Matches 1029	Conservative	0	Mismatches 3	Indels 1	Gaps 1
OY	26	ggtctgcgcgtctgagccgcgcgtctgtcgcgtctctctccctctgagccctgag	85		
Db	3	GGCTGGGGGCTGGGCGCGGGGCGCTGTGTGGCTTGTCTCTCTGGGCTTGGGCTGAG	62		
OY	86	caccgtgacgagcggtctcaactgtctcgggagacactaacccagcaacgagtgctgcca	145		
Db	63	CACCGTGACGGGGGCTCCACTGTGTGGGAGACCTAACCCAGCAACGACGGGTGCCA	122		
OY	146	cgaatgcagcgccagagcaacggyatgtgtgacgcgcctgcagcgctctccagaaacggtgtg	205		
Db	123	CGAGTGACAGGGCCAGGCAACGGGATGTGTAGCCGGCTGCAGCCCTCCCAACACGGTGTG	182		
OY	206	ccgtccgcctgcgcgcgcgcgtctcaacgaacgtgtgtcagctcccaagccgtgcgaacgcctg	265		
Db	183	CCGTCCGTCGGGGCGGGGCTTCTACACGACGTGTGCTCACTCCAAAGCCTGCACAGCCCTG	242		
OY	266	caagctgtgttaacctcagaagtgtggagtgtgacggaagcagcctgtgtcaagcgcacacagga	325		
Db	243	CACGTGTGTAACTCAGAAAGTGGAGTGTAGGCGGGAAGCAGCTGTGCACAGGCGACACAGA	302		
OY	326	cacagctctgcgcgctctcgcgcgcgcgcgaacccagccctctgacagctacaaagcctcgaggttga	385		
Db	303	CACACTGTGTCCGCTCCGGCGGGGACCCAGCCCTGTGACACTCTCAACCTGTGGAGTTGA	362		
OY	386	ctgtgcctccctctcctctcagggcacctctctcccaaggcgacacacagagccctgcaagccctg	445		
Db	363	CTGTGCCCCCTGTCCCTCCAGGGCACTTCTCCCAAGCGACAAACGACCTGCACAGCCCTG	422		
OY	446	gaccacactgcacactctgtcgt	505		
Db	423	GACCAACTGACACTTGTGGCTGTGGGAAACACACCCTGCAGCGCGGCAGCAATAAGCTCGGAGCG	482		
OY	506	aatctgt	565		
Db	483	AATCTGTGTAGGCAAGGAGAACCCCCCAGCCACGACGCCACGAGACCCCAAGGCGCCCCCGGCG	542		
OY	566	cagggccactcaatgtgtccagccaccctgtgaagctctgtgcccagaactcaacagagagccctcac	625		
Db	543	CAGGCGCATCACTGTGTCCAGGCCACTGTGAAGCTGTGGCCAGAACTCTCAGAGGACCTCTCCAG	602		
OY	626	ccgggcgcgtgtgaggtctcccccgggggcgcgtgtgcgtgtgcgcgcacactctgtgacctgtgt	685		
Db	603	CCGGCCCGGAGGAGTCCCGGGGGCGGTGCGGTGGCGCCATCTGTGGGCTGTGGGCTGTGT	662		
OY	686	gctgt	745		
Db	663	GCTGTGGGCTGTGTGGGCGCCCTTGGCCATCTGTGTGGCTGTGTACCTGTCCGAGAGGACCA	722		
OY	746	gaaggtgtcccccccgatgtcccaacaagcccccctgtggggaggaagcaatttccgaaccccatacca	805		
Db	723	GAGGCTGCCCCCGGATGCCACAAAGCCCCCTTGGGGAGGCAAGTTTCCGACCCCATTCAC	782		
OY	806	agaagagcagcgcgcgcacgcacacacttccacccctgtgccaagatctgacctgtggcccaaccaag	865		
Db	783	AAGAGGAGAGCGCGGACGCCCACTCCACCTGTGGCAAGATCTGACC-TGGGCCACCAAGG	841		
OY	866	tgtgacgtctgtgcccgcgcgcgcgcgtctgtgagcccggaaggtctgtctgtgcgcgcgcgcgcgcgc	925		
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LOCUS HSHOX40MR 1373 bp mRNA linear PRI 13-MAY-1994
DEFINITION H.sapiens mRNA for OX40 homologue.
ACCESSION X75962
VERSION X75962.1 GI:472957
KEYWORDS OX40 antigen.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE 1 (bases 1 to 1358)
AUTHORS Latza,U., Durkop,H., Schmittiger,S., Ringeling,J., Eitelbach,F.,
Hummel,M., Fomatsch,C. and Stein,H.
The human OX40 homologue: cDNA structure, expression and chromosomal
assignment of the ACT35 antigen
Eur. J. Immunol. 24 (3), 677-683 (1994)
94170844
JOURNAL 2 (bases 1 to 1373)
MEDLINE Latza,U.
REFERENCE Direct Submission
AUTHORS Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz,
JOURNAL Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG
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RESULT 5

AB003911 877 bp mRNA linear MAM 05-FEB-1999

LOCUS Rabbit mRNA for OX40 precursor, partial cds.

DEFINITION AB003911

ACCESSION AB003911.1 GI:2114107

VERSION OX40

KEYWORDS Oryctolagus cuniculus (sub-species: domesticus, strain: Chbb:HW)

SOURCE HTLV-I-transformed T cell line: H446 cDNA to mRNA.

ORGANISM Oryctolagus cuniculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

REFERENCE 1 (bases 1 to 877)

AUTHORS Isono,T.

TITLE Direct Submission

JOURNAL Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical Science, Central Research Laboratory; Seta Tsukinowachou, Otsu, Shiga 520-2192, Japan (E-mail: isono@shiga.ac.jp, Tel: 81-775-48-2308, Fax: 81-775-48-2048)

REFERENCE 2 (sites)

AUTHORS Isono,T. and Seto,A.

TITLE Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines



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JOURNAL Unpublished (1997)
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QY 94 cggggctccactgtgtgtgagcagcctaccacacagcagcagcgtgtgtcagagtgca 153
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QY 394 cctgcctccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 453
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LOCUS
DEFINITION Homo sapiens chromosome 1 clone RP5-902P8, *** SEQUENCING IN
PROGRESS ***, 4 unordered pieces.
ACCESSION AL162741
VERSION AL162741.24 GI:18643745
KEYWORDS HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eultheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (sites)
AUTHORS Harrison,E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 10, 2002 this sequence version replaced gi:18643745.
COMMENT ----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: dj902P8
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid, L08752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 16% of reads Chemistry:
Dye-terminator Big Dye; 83% of reads
Consensus quality: 110490 bases at least Q40
Consensus quality: 110677 bases at least Q30
Consensus quality: 110755 bases at least Q20
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Insert size: 160089; 6.7% error; agarose-fp
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coverage: 5.95x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
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* 42986 43085: gap of 100 bp
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* 54938 55037: gap of 100 bp
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  Location/Qualifiers

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Qy	980	gaatgctgcctctcggctctctctgaagtaagcaatgacataactctctgcgcccgaggagac	1039
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Qy	1040	acaaataaaaccttggcag 1058	
Db	9370	ACAAATAAAACCTTGGCAG 9388	

RESULT	8				
LOCUS	HSA277151				
DEFINITION	Homo sapiens ox40 gene for CD134 antigen, exons 1-7.	5150 bp	DNA	linear	PRI 05-JUL-2000
ACCESSION	AJ277151.1				
VERSION	AJ277151.1	GI:8926701			
KEYWORDS	CD134 antigen; OX40 gene; rat OX40 antigen homologue. human.				
SOURCE					
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
AUTHORS	Lacza, U., Dukup, H., Schuttiger, S., Ringeling, J., Etelbach, F., Hummel, M., Fonatsch, C. and Stein, H.				
TITLE	The human OX40 homolog: cDNA structure, expression and chromosomal assignment of the ACT35 antigen				
JOURNAL	Eur. J. Immunol.	24 (3),	677-683	(1994)	
MEDLINE	94170844				

REFERENCE	2 (bases 1 to 5150)
AUTHORS	Pankow, R., Dirkep, H., Latza, U., Krause, H., Kunzendorf, U., Pohl, T. and Buldione-Paus, S.
TITLE	The HTLV-I tax protein transcriptionally modulates OX40 antigen expression
JOURNAL	J. Immunol. 165 (1), 263-270 (2000)
MEDLINE	20318724
REFERENCE	3 (bases 1 to 5150)
AUTHORS	Pankow, R.
TITLE	Direct Submission
JOURNAL	University of Hospital Benjamin Franklin, Hindenburgdamm 30, 12200 Berlin, GERMANY
COMMENT	Related sequence X75962.
FEATURES	location/Qualifiers
SOURCE	1..5150
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	/db_xref="taxon:9606"
mRNA	join(1267..1437,1635..1757,2238..2429,2717..2783,3284..3480,3590..3718,3797..4096)
	/gene="ox40"
gene	1267..4096
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5' UTR	1267..1292
	/gene="ox40"
exon	1267..1437
	/gene="ox40"
	/number=1
CDS	join(1293..1437,1635..1757,2328..2429,2717..2783,3284..3480,3590..3718,3797..3867)
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	/note="rat OX40 antigen homologue"
	/codon_start=1
	/product="CD134 antigen"
	/protein_id="CAB96543.1"
	/db_xref="GI:8926702"
	/translation="MCVGARLGRGPCAALLILGLISTVYGLHCVDGYPSNDRCCHECRGNAGMSRSCSRNSQNTVCRPCGPRYNDVSSKRCPCITMCNLBSSSEKOLCTARQDTVICRCRAGTQPLDSTKPGVDCAPCPGHSFGEDNACKFWTCITLAGKHTLPASASDSDICEDRDEPAPQDETGGPARPRTVQTEFAMPRISQSPSTRPVEVPGGVAAALGLGLVIGLGLPLAILLALYLLRRDRLRPDAHKRPGGGSRFPDIOEQADAHSTLAKMI"
Intron	1438..1634
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	/number=1
exon	1635..1757
	/gene="ox40"
	/number=2
Intron	1758..2327
	/gene="ox40"
	/number=2
exon	2328..2429
	/gene="ox40"
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exon	2717..2783
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exon	3284..3480
	/gene="ox40"
	/number=5
Intron	3481..3589
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	/number=5
exon	3590..3718
	/gene="ox40"
	/number=6
Intron	3719..3796

[illegible]



Db 301 ACTGTCTGCAGATGTAGACGACGCCAACCTCGGACGAGGCGGTACAGCTTGA 360  
Qy gttgactgtccccctgtccccaagggaactcttcacaggcgacacagccgtcgaag 440  
Db 361 GTTGACTGTGTCCCTGCTCCTCTGCGCATTCTTCTCCAGGCAACACAGGCTGCAAG 420  
Qy 441 cccctggaacactgtacactgtgtgtggaacacacactgtcagccgagcaaatagctcg 500  
Db 421 CCGTGAGCAATGTAGCTTATCTGGAAGACAGACCCGCCACCCAGCCAGTACAGCTTG 480  
Qy 501 gacgcaatctgtgagaaagagagaccccccaagcagcagcccccaagagagaccagcc 560  
Db 481 GACGCAAGCTGTGAGAGAGAGAGAGCTCTGCGCACACTGCTGGAGAGACCCAGCGCTT 540  
Qy 561 ccgagcgaagccacatcactgtcagcccaactgaagcctgtgccccagaaactcaagagacc 620  
Db 541 ACATTCAAGGCCAACACACTGTCCAAATCCACACAGCTGTGCCCCAGACTTCTGAGTTGCC 600  
Qy 621 tccaccgagccgtgtgaggtgtcccgaggcggtgtgtgtgtgtgtgtgtgtgtgtgtgt 680  
Db 601 TCTCCACCCACCTGTGTGACTGCTGAGGGCCCTGCAATTTGCTGCTGAGGCTTGAGC 660  
Qy 681 ctgtgtctgt 740  
Db 661 -----CTGGGCTGT 714  
Qy 714 gaccagagctgt 800  
Db 715 GCTTGAGCAATTTG---CTTACACACTCCCAACCTTGTGTGGGAAACAGCTTCAGAGACCCG 771  
Qy 801 atccaagaag 860  
Db 772 ATCCAGAGAGAGAACACACAGACGACACTTACTGTGCGCAGAGATCTGAGCAATTAGTACAG 831  
Qy 861 caaggtgagagcgt 881  
Db 832 GAGTGTGATTTTATGGGACAG 852

## RESULT 11

LOCUS AR019521 1317 bp DNA linear PAT 05-DEC-1998  
DEFINITION Sequence 10 from patent US 5783665.  
ACCESSION AR019521  
VERSION AR019521.1 GI:3974635  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1317)  
AUTHORS Baum,P.R., Fanslow,W.C. III, Gayle,R.B. and Goodwin,R.G.  
TITLE Cytokine which is a ligand for OX40  
JOURNAL Patent: US 5783665-A 10-21-JUL-1998;  
FEATURES  
Location/Qualifiers  
OR.1317  
/organism="unknown"

BASE COUNT 322 a 417 c 337 g 241 t  
ORIGIN

Query Match 27.1%; Score 286.6; DB 6; Length 1317;  
Best Local Similarity 66.6%; Pred. No. 8.5e-35;  
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

Qy 87 accgtgaggggtccactgt 146  
Db 61 ACAGCAAGCGGCTCAACTGTGTAAACATACCTACCCAGTGTCACAAAGTGTGTGTGT 120  
Qy 147 gagtgcagggcagagcaagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 206  
Db 121 GAGTGCACGCGGCGCATGT 180  
Qy 207 cgtccgt 266

Db 181 CATCCGTGTGAGACTGCGCTTCTACAAATGAGCTGTCAATATGATACCTGCAGACAGTGT 240  
Qy 267 acgtgtgttaacctagaagatgt 326  
Db 241 ACACAGTGCACATCATGTGAGTGTGAAGTGAATCAAGCAAGAAATTTGACACATCTACGAT 300  
Qy 327 acagctgtgcgcgt 380  
Db 301 ACTGTCTGCAGATGTAGACGACGACCCAACTCCGAGACAGCGGCTACAAAGCTTGA 360  
Qy 381 gttgactgtccccctgtccccaagggaactcttcacaggcgacacagccgtcgaag 440  
Db 361 GTTGACTGTGTCCCTGCTCCTCTGCGCATTCTTCTCCAGGCAACACAGGCTGCAAG 420  
Qy 441 cccctggaacactgtacactgt 500  
Db 421 CCGTGAGCAATGTAGCTTATCTGGAAGACAGACCCGCCACCCAGCTTCTGAGTTGCC 480  
Qy 501 gacgcaatctgtgagaaagagagaccccccaagcagcagcccccaagagagaccagcc 560  
Db 481 GACGCAAGCTGTGAGAGAGAGAGAGCTCTGCGCACACTGCTGTGGAGACCCAGCGCTT 540  
Qy 561 ccgagcgaagccacatcactgtcagcccaactgaagcctgtgtgtgtgtgtgtgtgtgtgt 620  
Db 541 ACATTCAAGGCCAACACACTGTCCAAATCCACACAGCTGTGCCCCAGACTTCTGAGTTGCC 600  
Qy 621 tccaccgagccgtgtgaggtgtcccgaggcggtgtgtgtgtgtgtgtgtgtgtgtgtgt 680  
Db 601 TCTTACACCCACTTGT 660  
Qy 681 ctgtgtctgt 723  
Db 661 CCAGCACTGAGAGCGAGGCGCGCGCTGACGCTTCTCTTCTTC 703

## RESULT 12

LOCUS I14936 1317 bp DNA linear PAT 02-APR-1996  
DEFINITION Sequence 10 from patent US 5457035.  
ACCESSION I14936  
VERSION I14936.1 GI:1249844  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1317)  
AUTHORS Baum,P.R., Fanslow,W.C. III, Gayle,R.B. and Goodwin,R.G.  
TITLE Cytokine which is a ligand for OX40  
JOURNAL Patent: US 5457035-A 10-10-OCT-1995;  
FEATURES  
Location/Qualifiers  
OR.1317  
/organism="unknown"

BASE COUNT 322 a 417 c 337 g 241 t  
ORIGIN

Query Match 27.1%; Score 286.6; DB 6; Length 1317;  
Best Local Similarity 66.6%; Pred. No. 8.5e-35;  
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

Qy 87 accgtgaggggtccactgt 146  
Db 61 ACAGCAAGCGGCTCAACTGTGTAAACATACCTACCCAGTGTCACAAAGTGTGTGTGT 120  
Qy 147 gagtgcagggcagagcaagagatgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 206  
Db 121 GAGTGCACGCGGCGCATGT 180  
Qy 207 cgtccgt 266  
Db 181 CATCCGTGTGAGACTGCGCTTCTACAAATGAGCTGTCAATATGATACCTGCAGACAGTGT 240

[illegible]

LOCUS	AR019518	618 bp	DNA	linear	PAT 05-DEC-1998
DEFINITION	Sequence 6 from patent US 5783665.				
ACCESSION	AR019518				
VERSION	AR019518.1	GI:3974632			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unknown.				
REFERENCE	Unclassified.				
AUTHORS	1 (bases 1 to 618)				
TITLE	Baum, P.R., Fanslow, W.C. III, Gayle, R.B. and Goodwin, R.G.				
JOURNAL	Cytokine which is a ligand for OX40				
FEATURES	Patent: US 5783665-A 6 21-JUL-1998;				
source	Location/Qualifiers				
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	/organism="unknown"				
BASE COUNT	148 a	187 c	151 g	132 t	
ORIGIN					
Query Match	26.8%; Score 283.2; DB 6; Length 618;				
Best Local Similarity	70.6%; Pred. No. 3.4e-34;				
Matches 394;	Conservative 0; Mismatches 158; Indels 6; Gaps 1;				
Db	87 accgtacagggtcctacactgtctcggggacacactaccccaacagaccggtgtcgcac	146			
61 ACAGCAAGCGGGCTCACTGTGTTAAACATACCTACCCACAGTGCACACAGTGCCTGCT	120				
Db	147 gactgacaggccaaggcaacgagatggtgacgcgtgacgcgctcccaagaacagtgctgc	206			
121 GAGTCCAGCCAGCGGCATCATGTATGCTGAAACCGCTGTATCATACCAAGGATACCTGATGT	180				
Db	207 cgttcgtgcgggcccgggtcttctacaaacgacgtgtgtcagctcccaagcgtgtgcaagccctgc	266			
181 CATCCGTGTGAGACTGCTTCTACATGAACTGCTCAATTATGATACCTGCACAGCAGTGT	240				
Db	267 acgctggttaacctcagaagatgggagtgtaggggaagcagcgtgtgacagggcccaacagac	326			
241 ACACAGTCAACCATCGACAGTGAAGTGAAGTCAACTCAAGAAATTGGACACACTTACTGAGAT	300				

QY	327	acagctctgcgcctgcgcgggacggacacccgcctggg-----cagctaaagccttga	380
Db	301	ACTGCTCAGACATGATGAGACACAGCACCCACACTCCGGCAGACAGGGGCTTACAACTTGA	360
QY	381	gttgacgtgtgcctccctgcctcccaaggacattctctccaaagcgacacacagccttgaag	440
Db	361	GTTCACGTGTTCCCTCGCCCTCTCTGGCCACCTTTTCTCAGGCGACACACAGGCCCTGCAAG	420
QY	441	cccttgaccacacatgcaccttgtcttgaagacacaccccttgcgcggacgaacatagtctcg	500
Db	421	CCCTGGACCAATTGTGACTTATCTGTGAAAGCAGACCCGCCACCCAGCCAGTGACAGCTTG	480
QY	501	gaacgaacatctgttgaagaagggaaaccccccaagccaaagcagccccaaggaaccagggcccc	560
Db	481	GACGCAAGTCTGTGAGAGACAGAAAGCCTCTGTGGCCACACTGCTTGTGGAGACCCAGGCGCTT	540
QY	561	ccggcagcgcacatcacttctcagcccaactgaagccttgaagccttgcgcgaacatcacaaggaacc	620
Db	541	ACATTCAGGSCCAACACGTGCCAATTCACACACAGTCTGAGCCACGAGCATTTGAGTTGGCC	600
QY	621	tccaacggcccgctgtgag	638
Db	601	TCTACACCCACACTTGGTG	618

[illegible]



Db	361	GTGACGTGTGTTCCCTCGCCCTCCGACACTTTTCTCCAG6CAACACAGGCGCTGGAAG	420
OY	441	cccttggaccacacttgcaccttggcttggtaagacaccccttgcagccggtccagaatagtctg	500
Db	421	CCCTGGACCAATTTTACTTATTCTTGAAACACAGCCGCCACCCAGCCATGACAGCTTG	480
OY	501	gaaccaatctgttgaaggacaggaagccccccagccacgcagcccccagagagacacgaaggcccc	560
Db	481	GACCGACGTCTGTGAGGACAGAAAGCCTCTCTG6CCACACTGCTCTTG6GAGACCCAGCGCCT	540
OY	561	ccggaccagcccatcactgttctcagcccaacttgaagctcttggcccaagaaacttacaagggacc	620
Db	541	ACATTTCAGGCGCAACACACTGTCTCAATCCACACACACTGTGCGCCAGAGACTTCTGAGTTGCC	600
OY	621	tccagccgggtcccttggag	638
Db	601	TTCTACACCCACTTTGGTG	618

RESULT	15			
AX251336/c				
LOCUS	AX251336	6080 bp	DNA	linear
DEFINITION	Sequence 304 from Patent WO0168912.			PAT 05-OCT-2001
ACCESSION	AX251336			
VERSION	AX251336.1			
KEYWORDS	GI:15984759			
SOURCE	.			
ORGANISM	synthetic construct. synthetic construct. artificial sequence. 1 (bases 1 to 6080) Olek,A., Piepenbrock,C. and Berlin,K. Diagnosis of diseases associated with tumor suppressor genes and oncogenes Patent: WO 0168912-A 304 20-SEP-2001; Epigenomics AG (DE)			
JOURNAL	location/Qualifiers			
FEATURES	1..6080			
source	/organism="synthetic construct" /db_xref="taxon:32630" /note="Chemically treated genomic DNA (Homo sapiens)"			
BASE COUNT	1124 a 278 c 1963 g 2715 t			
ORIGIN				

Query Match	11.8%	Score 12.4	DB 6	Length 6080
Best Local Similarity	74.8%	Pred. 3.7e-10		
Matches	169	Conservative	0	Mismatches 55; Indels 1; Gaps 1;
QY	832	ccctgagccaagaatctgacacttgggcccacaaagtgtgacgctgggcccgcgcagcttga	891	
Db	6080	CCCTAACCAAAATCTTAACCC-TAAACCCCAAAAATAAACGCTAATAACCCGCAACTTAA	6022	
QY	892	gcccgggaagggtctgtgtggcgagcagggcaggtgtcagcgcgcttcgcgcgcagcgtcct	951	
Db	6021	ACCCGAAAAATCTTAATAAGCAACAAACAAATATACAAACCGCTACCCCGCACGCTCT	5962	
QY	952	gggcaactctgcacgcgttctagtgtagcgcgatgtgcctcgcgcctctctgtcactgaty	1011	
Db	5961	AAACCAACTCTACACCGTTCTTAATATACGATTAACCTACGACGACGCTCTACTTACGTATA	5902	
QY	1012	ccatgcataacctcctgtgcccgcgaggacccaataaaaccttggca	1057	
Db	5901	CCATGCATACGCTCTACCCCGGGAACCAACATATAAAACCTTTAACA	5856	

Search completed: June 18, 2002, 18:44:09  
Job time: 14967 sec

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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 1939.35 Seconds  
(without alignments)  
7363.178 Million cell updates/sec

Title: US-09-852-845-1  
Perfect score: 1058  
Sequence: 1 cagcagagcagcagatgtgc.....cacataaacacctgycag 1058

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

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EST.\*  
1: em\_estba.\*  
2: em\_esthum.\*  
3: em\_estin.\*  
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5: em\_estov.\*  
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7: em\_estro.\*  
8: em\_hlc.\*  
9: gb\_est1.\*  
10: gb\_est2.\*  
11: gb\_hlc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	615.6	58.2	844	9	AT1738634
2	564	53.3	743	10	BI833441
3	540	51.0	569	10	BG236062
4	526.4	49.8	544	10	BF063899
5	498.4	47.1	893	10	BI911081
6	495	46.8	512	10	BE349098
7	417.6	39.5	471	9	AM293499
8	352.2	33.3	668	9	AT1991307
9	331.6	31.3	398	9	AA970291
10	305.4	28.9	353	9	AM290885
11	298.2	28.2	347	9	AI452801
12	289.4	27.4	393	9	AA306055
13	282	26.7	630	9	AA501118
14	214.8	20.3	609	9	AT323590
15	206.4	19.5	247	9	AI914208
16	178.6	16.9	198	9	AM591834
17	145.2	13.7	172	10	BI824093

c	18	139	13.1	560	9	AM743856
	19	135.4	12.8	511	10	BM285756
	20	130	12.3	423	9	AA110765
	21	130	12.3	459	9	AT323199
	22	92	8.7	92	10	BI821828
	23	85.4	8.1	414	9	BE095512
	24	81.4	7.7	459	9	AM744325
	25	74.6	7.1	925	12	CNS0091P
	26	74.6	7.1	1389	10	BG624255
	27	70.4	6.7	925	12	CNS0091P
	28	68.6	6.5	935	12	CNS006X
	29	65.2	6.2	888	12	AG030591
	30	64.8	6.1	776	12	CNS010RY
	31	64.8	6.1	932	12	CNS00720
	32	64.2	6.1	935	12	CNS006X
	33	64.2	6.1	1203	12	CNS015Y4
	34	63.4	6.0	885	12	AG159162
	35	63.2	6.0	313	9	BI164410
	36	63	6.0	1137	10	BG809979
	37	61.6	5.8	1389	10	BG624255
	38	61	5.8	911	12	AG043617
	39	60.8	5.7	691	12	AG171171
	40	60.8	5.7	724	12	AG171201
	41	60.8	5.7	978	12	AG030617
	42	60.6	5.7	613	12	AG043036
	43	60.6	5.7	817	12	AG140822
	44	60.6	5.7	1100	12	AG161988
	45	60	5.7	1101	12	CNS01523

#### ALIGNMENTS

RESULT 1  
AT1738634/c 844 bp mRNA linear EST 20-DEC-1999  
LOCUS willid02.x1 NCI-CGAP.C016 Homo sapiens CDNA clone IMAGE:238923 3'  
DEFINITION similar to SW:OX40.HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains  
MER22.t3 MSRI repetitive element ;, mRNA sequence.

ACCESSION AT1738634  
VERSION AT1738634.1 GI:5100615  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 844)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
AUTHORS National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
TITLE Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,  
Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
Clone Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
[www-bio.lnl.gov/dbtrp/image/image.html](http://www-bio.lnl.gov/dbtrp/image/image.html)  
Insert Length: 1075 Std Error: 0.00  
Seq primer: -40up from Gibco  
High quality sequence stop: 452.  
Location/Qualifiers

#### FEATURES

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/db\_xref="taxon:9606"  
/clone="IMAGE:238923"  
/clone\_lib="NCI-CGAP.C016"  
/tissue\_type="colon tumor, RER+"  
/lab\_host="DH10B"  
/note="Organ: colon; Vector: pT7T3D-Pac (Pharmacia) with a

modified polylinker; Site\_1: Not I; Site\_2: Eco RI; Plasmid DNA from the normalized library NCI\_CGAP\_C010 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (clonoids 1057416-1061255, and 1145584-1145351). Subtraction by Bento Soares and M. Fatima Bonaldo. "

BASE COUNT 139 a 245 c 302 g 154 t 4 others  
ORIGIN

Query Match 58.2%; Score 615.6; DB 9; Length 844;  
Best Local Similarity 93.6%; Pred. No. 3.4e-98;

Matches 661; Conservative 0; Mismatches 43; Indels 2; Gaps 2;

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OY 353 ccagcccccgtgagcgtctaaagcctgagtgactgtgcccctcctcctcagggagcact 412
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 704 CCCACCCCTGCGCAGTTACATAGCTGGAG-TGCTGTGTCACCTGCCCTTACAGTGCATTTC
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 413 ctcccccagggcgaacaacagagcctgcaagcctgagaccactgacacttgctggagaaga 472
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 645 TCCCGCAGTGAACACAGGCGCTTCCAAAGCAGTGAACCACTGGACTTGGNTGGAGCGCA 586
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 473 caacctgcaagccggcgaacaataagctcgagcgaatctgtgagagcagagcccccagc 532
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DB 585 CACCATGCAAGCGCGGCGGCAATAGCTCGGACCAATCTGTGAGAGACAGGACCCCCACAC 526
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OY 533 cagcagcccccaggaagaccagagcccccggcagccagccatcactgtctcagccacatga 592
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 525 CACGCAAGCCCCAGAGACACCAGGCCCCCGGCGAGGCCCATCTGTCCAGCCCAANTBA 466
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OY 593 agcctggcccaagaacctcacaaggaacctcacaacccggccgtggaggttcccgaggcg 652
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DB 465 ACGNTGGCCCAACACTCACAGGAGACCTCCACCCGCGCCGTGGAGAGTCCCGGGGGCGCG 406
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 653 tggcgttgcgcgaatcctgagcctgagcctgtgtgctggggcgtgagggcccccctggcat 712
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 405 TCGCGTTGCGCGCATCTCTGGCTTGCGCTGGGTGCTGGGGCTGTGGGCCCTTGCCAT 346
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 713 cctgtcgtgcccctgtacactcctcgcgagagagacagagcctgcccgcgaatgaccaagaac 772
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 345 CCTGCTGCGCCCTGTACTCTCTCGGAGGAGACCAAGAGCTGCCCGCGATGCCACAGGC 286
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 773 cccctggggaggagcagttctccggaaccccaaccgaagagagcagggccgaccccaactcac 832
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 285 CCGTGGGGGAGGAGAGTTCGCGACCCCATCCAAAGAGAGAGGCGGACGACCTCCAC 226
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 833 ccttgcgcaagatctgaaccttggcgcgaaggtgagagcctgagcccgccagggcgtgag 892
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 225 CCGTGGCCAAAGATTGTGAC-TGGGCCCAACCAAGGTGAGCTTGCGGCCCGCCAGGCTGGAG 167
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 893 ccgaggaggtctcgtcgtgagcagagcaggtgcagcgcctgcccgcgacagctcctcg 952
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 166 CCGGAGGGGTCTGCTGGGGGAGAGGAGGTGACAGCGCGCTGCCCGCGCACAGCTGCTG 107
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 953 ggcacaactctgacagcttctaggtgcgaatggtcgtccctcggcctctcgtcttaagatatt 1012
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 106 GGCCAACTCTGACAGCTTCTAGGTGCCGATGCTGCTCGGCTCTCTCTTACGATATGC 47
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 1013 catgtatactctcgtccgcgagagacacaataaacttggcag 1058
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 46 CATGCACTACTCTCTGCGCGGAGACCAATMAAAACCTTGGCAG 1
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
```

RESULT 2  
BI833441 743 bp mRNA linear EST 04-OCT-2001  
LOCUS 60308095F1 NIH\_MGC\_120 Homo sapiens cDNA clone IMAGE:5227199 5',  
DEFINITION mRNA sequence.  
ACCESSION BI833441  
VERSION 81833441.1 GI:15944991  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 743)  
AUTHORS NIH-MGC <http://mgi.ncl.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
CONTACT: Robert Strausberg, Ph.D.  
COMMENT Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Life Technologies, Inc.  
CDNA Library Preparation: Life Technologies, Inc.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: LLM11571 row: m column: 24  
High quality sequence stop: 659.

FEATURES  
source  
Location/Qualifiers  
1..743  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:5227199"  
/clone\_11b="NIH\_MGC\_120"  
/lab\_host="DH10B"  
/note="Organ: pooled pancreas and spleen; Vector:  
pCMV-SPORT6; Site\_1: NotI; Site\_2: EcoRV (destroyed); RNA  
source anonymous pool of spleen and pancreas from 28 yo  
male. Library is oligo-dT primed and directionally cloned  
(EcoRV site is destroyed upon cloning). Average insert  
size 1.5 kb. Insert size range 1-2.5 kb. Library is  
normalized and enriched for full-length clones and was  
constructed by C. Gruber (Invitrogen). Research Genetics  
tracking code 025. Note: this is a NIH-MGC Library."

BASE COUNT 135 a 275 c 235 g 98 t  
ORIGIN

Query Match 53.3%; Score 564; DB 10; Length 743;  
Best Local Similarity 95.2%; Pred. No. 3.5e-89;  
Matches 668; Conservative 0; Mismatches 25; Indels 9; Gaps 8;

```

OY 353 ccagcccccgtgagcgtctaaagcctgagtgactgtgcccctcctcctcagggagcact 412
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 1 CAGGCCCTGAGACAGCTTAAAGCTGTGAGTGTGCTGCCCTGCCCTCCAGAG-ACCT 59
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 413 ctcccccagggcgaacaacagagcctgcaagcctgagaccactgacacttgctggagaaga 472
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 60 CTCGCCAGGCGACACCAAGGCTCGAAGCCCTGACCAACTGACCTTGGCTGGAGACA 119
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 473 caacctgcagccggcagcaatagctcagagcgaatctgtgagagcagagaccccccagc 532
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 120 CACCTGCAAGCGCGGAGCAATAGCTCGAGCGCAATCTGTGAGAGACAGGAGACCCCGACAG 179
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 533 cagcagcccccaggaagaccagggcccccggcagagcccatcactgtctcagccacatga 592
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 180 CACGCAAGCCCCAGAGAAACCA-GGCCCCCGGCGAGGCCCATCTACGTCCAGGCCACTGA 238
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 593 agcctggcccaagaacctcacaaggaacctcacaacccggccgtggaggttcccgaggcg 652
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 239 AGCTTGCCCAAGACTTCAAGGAGACCTTCACCCGCGCGTGGAGTCCCGGGGGCGG 298
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 653 tggcgttgcgcgaatcctgagcctgagcctgtgtgctggggcgtgagggcccccctggcat 712
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 299 TGGGTTGCGCGCATCTCTGGCTTGCGCTGGGTGCTGGGGCTGTGGGCCCTTGCCAT 358
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 713 cctgtcgtgcccctgtacactcctcgcgagagagacagagcctgcccgcgaatgaccaagaac 772
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
DB 359 CTTGCTGCGCCCTGTACTCTCTCGGAGGAGACCAAGAGGCTG-CCCGCGATGCCCAAGGCC 417
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
OY 773 cccctggggaggagcagttctccggaaccccaaccgaagagagcagggccgaccccaactcac 832
    || |||| | |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
```

Db 418 CCTGGGGGAGGAGCTTCCGACCCCATCATCAAGAGAGAGAGGCGACGCCACTCCAA 477

Qy 833 cctggcaagaatctgaccttgagccaccacaagtggagcctgggccccgcagagctgag 892

Db 478 CCTGGCCCAAGATCTGACC-TGGGCCACCAAGGTGGAGCTGGGCCCGCCGACGGGTGAG 536

Qy 893 cccgagaggtctgtggtgagcagagggcagag--tgagagccgctcgtccgcacagctcc 950

Db 537 CCGGAGGGCTGTGGTGGGCGAGAGGGGAGGTTGACAGGCTGCTG--CCCGGACAGCTCC 595

Qy 951 tgggcaactctgacagcttcta-gtgcgagtgtgctcctcgagctctctgtactgta 1009

Db 596 TGGGCAACTCTGGACCGCTGTAGGGTGCCTGATGGCTGGCTCTCTGTGTACGTA 655

Qy 1010 tgcatactctgctccgcgagcagcaataaanaac 1050

Db 656 TGCATGTGCATTAATCTCTGGCCCGGAGGACAGCAATTAAC 697

RESULT 3  
Bg236062/c  
LOCUS  
DEFINITION Bg236062 569 bp mRNA linear EST 12-FEB-2001  
naft22a07.x1 Soares\_NPBMC Homo sapiens CDNA clone IMAGE:4141716 3'  
similar to SW:OX40\_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains  
MER22.t1 TARI repetitive element ; mRNA sequence.

ACCESSION Bg236062  
VERSION Bg236062  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheraia; Primates; Catarrhini; Homindae; Homo.  
1 (bases 1 to 569)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: M. Bento Soares, Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima  
Bonafido, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN),  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
info@image.jnl.gov  
Seq primer: -400P from Glibco  
High quality sequence stop: 478.  
Location/Qualifiers  
1. 569  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4141716"  
/clone\_id="Soares\_NPBMC"  
/tissue\_type="Lymphocyte"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: blood; Vector: pT7MD-pac; site:1: NotI;  
site:2: EcoRI; 1st strand CDNA was primed with a Not I -  
oligo(dT) primer [5'  
TGTTCACATCTGAAGTGGAGCGCGCGGCTTTTTTTTTTTTTTTTTTTTTTTTTTTTT  
3']; double-stranded CDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not  
I and Eco RI sites of the modified pT73 vector. Library  
is normalized; constructed in the laboratory of M. Bento  
Soares (University of Iowa)."

BASE COUNT 78 a 179 c 223 g 89 t

ORIGIN

Query Match 51.0%; Score 540; DB 10; Length 569;  
Best Local Similarity 99.8%; Pred. No. 5.2e-85;  
Matches 551; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 507 atcttgagagcagggaccacccccaagccacgcagagccccaagagaccagggcccccggcc 566

Db 509 ATCTGTGAGACAGGAGACCCCCCACCACGACAGCCCCAGAGACCCAGGCCCCCGGCGC 510

Qy 567 aggcccaatcactgtlccaaagccactgaagccttgagcccaagaactcaagaagacccctcaac 626

Db 509 AGGCCATACATGTCACACCCACTGAACCTTGCGCCCAACACTCAAGAGAACCTTCCACC 450

Qy 627 cggccgctgagaggtcccccgggggcccgtgaggttcgcgcacatcctgagccttgagctg 686

Db 449 CGGCCCTGTGAGGTCCCGGGGGCGCTGCGTTCGCGCATCTTGCGCTGGGCTTGCTG 390

Qy 687 ctggagctgctgagccccccttgacatctgctgagccctgacatcctgctccgagagagcag 746

Db 389 CTGGGGCTGCTGGGCCCTTGCGCATCTGCTGCGCTGTGCTCTCGGAGGAGACAG 330

Qy 747 agactgtcccccagatgcccacaagccccccttgaggagagcagtttccgagaccacca 806

Db 329 AGGCTGCCCGCCGATGCCACAGCCCTGGGGAGGACAGTTTCGGACCCCATCCAA 270

Qy 807 gagagagcagggccgagagcccaactccaccccttgagcagaatctgaccttgagcccaaggt 866

Db 269 GAGGAGCAGGCGGAGCGCCACTCCACCTGGCCAAAGATCTGACC-TGGGCCACCAAGCT 211

Qy 867 ggaagctggcccccgccagagctgagagccgagaggtctgctgagggcagcagagagctgc 926

Db 210 GGACGCTGGCCCCCGCCAGAGCTGGAGGCCGAGAGGTCTGCTGGGAGCAGGACAGGCTGC 151

Qy 927 aggcgcctgcccccgccagagcctcctgtggccaactctgacagctgttctagatgctgagct 986

Db 150 AGGCGCGCTGCCCGCCGACGCTCTGGGCAACCTGTGACCGTTGTAGTGCGCATGGCT 91

Qy 987 gcttcgagctctctgtcttaagctatgcatgtatactctcgtcccgaggagacaaataa 1046

Db 90 GCCTCGGCTCTGCTTACGTATGCATTAATGCTCTCCGCCGCGGACACAAATPA 31

Qy 1047 aaaccttgccag 1058

Db 30 AAACCTTGGCAG 19

RESULT 4  
BF063899/c  
LOCUS  
DEFINITION BF063899 544 bp mRNA linear EST 16-OCT-2000  
7hp0a10.x1 NCI-CGAP\_CO16 Homo sapiens CDNA clone IMAGE:3323226 3'  
similar to SW:OX40\_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains  
MER22.t1 PTR5 repetitive element ; mRNA sequence.

ACCESSION BF063899  
VERSION BF063899  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheraia; Primates; Catarrhini; Homindae; Homo.  
1 (bases 1 to 544)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.  
Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN, send email to:  
info@image.jnl.gov  
Seq primer: -400P from Glibco  
High quality sequence stop: 423.  
Location/Qualifiers

FEATURES









0y	940	cgccacgctcctctggcgcaactctgacacgcttctagtctcgatgctctcccgctctc	999
Db	144	CCCCAGTTCCTTGGGGCCAAATTTTGGCCCGCTTTTACGTCCGATGGCTCCTCCGGCTTTT	85
0y	1000	tgcctacgtatgcacatgatatacctctgccccgcggagacacaaataaaccttgccag	1058
Db	84	TGCTTACGTATGCGCATGTCATACCTCTCTCCCGCGGAGCCCATTAACCTTGGCAG	26
RESULT	9		
AA970291/c			
LOCUS			
DEFINITION	AA970291	398 bp	mRNA
ACCESSION	op09ph05.s1	NCI_CGAP_kid6	Homo sapiens cDNA clone IMAGE:1575225 3'
VERSION	AA970291		similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;, mRNA
KEYWORDS	sequence.		
SOURCE	AA970291.1	GI:3145804	
ORGANISM	human.		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (bases 1 to 398)		
COMMENT	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: cgapbs-remail.nih.gov		
	Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.		
	Emmert-Buck, M.D., Ph.D.		
	CDNA Library Preparation: Stratagene, Inc.		
	CDNA Library Arrayed by: Greg Lennon, Ph.D.		
	DNA Sequencing by: Washington University Genome Sequencing Center		
	clone distribution: NCI-CGAP clone distribution information can be		
	found through the I.M.A.G.E. Consortium/ILMIL at:		
	<a href="http://www-bio.llnl.gov/bdpr/Image/Image.html">www-bio.llnl.gov/bdpr/Image/Image.html</a>		
	Seq primer: -40ml3 fwd. RT from Amersham		
	High quality sequence stop: 180.		
FEATURES			
Source	Location/Qualifiers		
	1..398		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:1575225"		
	/clone_lib="NCI-CGAP_kid6"		
	/sex="mixed"		
	/tissue_type="Kidney tumor"		
	/lab_host="SOIR (kanamycin resistant)"		
	/note="Organ: kidney; Vector: Bluescript SK-; Site:1;		
	Ecobi: Site_2: XhoI; Cloned unidirectionally. Primer:		
	Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'		
	GAAATCGGACGAG 3' 3' adaptor sequence: 5'		
	CCTCAGATGTTTTTTTTTTTTT 3' Average insert size: 1.0 kb."		
ORIGIN			
	61 a 125 c 146 g 66 t		
Query Match	31.3%	Score 331.6;	DB 9; Length 398;
Best Local Similarity	94.0%;	Pred. No. 1.3e-48;	
Matches 378;	Conservative	0; Mismatches 19;	Indels 5; Gaps 3;
0y	648	gaccctgsgatggcgcacatcctctgagcctgagcctgagcctgagcctgagcctctg	707
Db	398	GGGCGCATGGTTGCGCCATCTGGGCGCTGGGCGCTGGTCTGAGCTACTGCGCCCTG	339
0y	708	gccactctgctggcccttacctgctccggagggagacagagcttcccccgatgcc-a	766
Db	338	GCAATCTGCTGGGCGCTTACCTGCTGCCGGAGGACACAGAGCTGCCCCCGATGCCAA	279
0y	767	caagccccctggggagagcagttctcgagaccccccatccaagaagagcagccgaccca	826
Db	278	CAAGACCCCTGGGGAGGACAGTTTCCGACCCCAATCCAGAGGAGGAGCGGCGAGCCCA	219

QY	827	ctccaccctgaccaagatctgaactcttgagccaccaccaaggtggaagcttgagcccgccag	886
Db	218	ctccaccctgaccaagatctgaactcttgagccaccaccaaggtggaagcttgagcccgccag	160
QY	887	ctggagagcccgaggggtctgcttgaggagagagagggaggggtgcaagccgcttgcccgccag	946
Db	159	ctggagagcccgaggggtctgcttgaggagagagagggaggggtgcaagccgcttgcccgccag	100
QY	947	ctccctgggccaactctgacccgtcttaagtgtcgagatgagcttcctcgagctctcttacc	1006
Db	99	ctccctgggccaactctgacccgtcttaagtgtcgagatgagcttcctcgagctctcttacc	43
QY	1007	gtatgcacatgaatacctctctgcccgcgggacacataaaa	1048
Db	42	gtatgcacatgaatacctctctgcccgcgggacacataaaa	1
RESULT	10		
LOCUS	AM290885/c	353 bp	linear
DEFINITION	UI-H-B12-aggd-b-03-0-UI.s1 NCI_CGAP_Sub4 Homo sapiens	CDNA clone	
ACCESSION	AM290885		
VERSION	AM290885.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 353)		
TITLE	NCI-CGAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .		
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP),		
COMMENT	Tumor Gene Index		
	Unpublished (1997)		
	Contact: Robert Strausberg, Ph.D.		
	Email: <a href="mailto:cgapsb@remail.nih.gov">cgapsb@remail.nih.gov</a>		
	The sequence contained an oligo-dT track that was present in the		
	oligonucleotide that was used to prime the synthesis of first		
	strand cDNA and therefore this may represent a bonafide poly A		
	tail. CDNA Library Preparation: M.B. Soares Lab Clone distribution:		
	NCI-CGAP clone distribution information can be found through the		
	I.M.A.G.E. Consortium/LNLT at:		
	<a href="http://www.bio.lnlt.gov/bbrp/image/image.html">www.bio.lnlt.gov/bbrp/image/image.html</a>		
	Seq primer: M13 Forward		
	POLYA-Tes.		
FEATURES	Location/Qualifiers		
source	1..353		
	/organism="Homo sapiens"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:2723669"		
	/clone_lib="NCI_CGAP_Sub4"		
	/lab_host="DH10B (Life Technologies)"		
	/note="Vector: pRT3D-Pac (Pharmacia) with a modified		
	polylinker. Site.1: Not I; Site.2: Eco RI; The		
	NCI_CGAP_Sub4 library is a subtracted library derived from		
	the NCI_CGAP_Sub2 library which is a subtracted library		
	derived from the NCI_CGAP_Sub1 library, which is a		
	subtracted library derived from B1. B1 constitutes a		
	mixture of 21 normalized or subtracted NCI_CGAP		
	libraries: NCI_CGAP_C04, NCI_CGAP_Pr22, NCI_CGAP_Pr28,		
	NCI_CGAP_C010, NCI_CGAP_C016, NCI_CGAP_Kid5,		
	NCI_CGAP_Kid12, NCI_CGAP_Kid3, NCI_CGAP_Kid11,		
	NCI_CGAP_Lym2, NCI_CGAP_Pr2, NCI_CGAP_C08, NCI_CGAP_C11,		
	NCI_CGAP_La12, NCI_CGAP_Brn13, NCI_CGAP_Lu5,		
	NCI_CGAP_La24, NCI_CGAP_Lu19, NCI_CGAP_G04, NCI_CGAP_G06,		
	NCI_CGAP_Brn25. These 21 libraries were pooled and a		
	single-stranded DNA preparation of the resulting mixture		
	was used as a tracer in a subtractive hybridization with		
	a driver whose composition is detailed below:		
	NCI_CGAP_Kid3 pool 1 : LHAM 3334-3337, 3682-3683,		
	3798-3803 (IMAGE ClonesIDs 1322376-1323911,		
	1456008-1456775, 1500552-1502855) NCI_CGAP_Kid5 pool 1 :		



FEATURES	BASE COUNT	ORIGIN
Source	73 a 151 c 124 g 45 t	
Location/Qualifiers		
1. 393		
/organism="Homo sapiens"		
/db_xref="ATCC (inhost):160207"		
/db_xref="taxon:9606"		
/clone_lib="Jurkat T-cells VI"		
/cell_type="T-lymphocyte"		
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"		
Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
Seq primer: M13 Reverse.		
Location/Qualifiers		
1. 393		
/organism="Homo sapiens"		
/db_xref="ATCC (inhost):160207"		
/db_xref="taxon:9606"		
/clone_lib="Jurkat T-cells VI"		
/cell_type="T-lymphocyte"		
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"		
Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
Seq primer: M13 Reverse.		
Location/Qualifiers		
1. 393		
/organism="Homo sapiens"		
/db_xref="ATCC (inhost):160207"		
/db_xref="taxon:9606"		
/clone_lib="Jurkat T-cells VI"		
/cell_type="T-lymphocyte"		
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI"		
Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
Seq primer: M13 Reverse.		
Location/Qualifiers		
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/organism="Homo sapiens"		
/db_xref="ATCC (inhost):160207"		
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Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
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Location/Qualifiers		
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Email: arkerlavet@tigr.org		
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Seq primer: M13 Reverse.		
Location/Qualifiers		
1. 393		
/organism="Homo sapiens"		
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Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
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Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
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Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
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Seq primer: M13 Reverse.		
Email: arkerlavet@tigr.org		
For clone availability, additional sequence and expression information related to this EST, please check the TIGR Human Gene Index ( <a href="http://www.tigr.org/bgi/bgi.html">http://www.tigr.org/bgi/bgi.html</a> )		
Seq primer: M13 Reverse.		
Location/Qualifiers		
1. 393		
/organism="H		

ACCESSION	sequence.
VERSION	AA501118
KEYWORDS	AA501118.1 GI:2236085
SOURCE	EST.
ORGANISM	house mouse. Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS	1 (bases 1 to 630) Marra,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubouque,T., Geisels,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,B., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Thiesing,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HHMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Marra M/Mouse EST Project WashU-HHMI Mouse EST Project Washington University School of Medicine 444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@watson.wustl.edu This clone is available royalty-free through LLNL ; contact the IMAGE Consortium ( <a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a> ) for further information. MG1:503921 Seq primer: -28ml3 rev2 ET from Amersham High quality sequence stop: 196. Location/Qualifiers 1..630 /organism="Mus musculus" /strain="C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:851769" /clone_lib="Soares_mammary_gland_NbMMG" /sex="male" /tissue_type="mammary gland" /lab_host="DHL10B" /dey_stage="4 weeks" /note="Organ: mammary gland; Vector: pT7T3D-Pac (Pharmacia ) with a modified polylinker; Site.1: Not RI; Site.2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(ct) primer [5', TGTTCAACAATCTGAAGTGGCGCCGCCGAGATGTTCCTTTTTTTTTCCTTTTTTTT T 3']; double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT7T3 vector. RNA provided by Dr. Minoru Ko, Wayne State Univ. library constructed and normalized by Bento Soares and M.Patima Bonaldo."
BASE COUNT	144 a 196 c 152 g 138 t
ORIGIN	
Query Match	26.7%; Score 282; DB 9; Length 630;
Best Local Similarity	69.0%; Pred. No. 6.2e-40;
Matches 436; Conservative	0; Mismatches 180; Indels 16; Gaps 3;
Db	210 ccgttcggcgccgagcttccacaagaagctgtgcacgtcctaagcgttgtagaccctgcacg 269
Db	9 CAGGGGTGACTGGCTTCTTCAATATAAGCTGCATTATATGATACCTGGCAGAGTGTACA 68
Db	270 ttgttaacctcaagaagtggagttgaaggaaagcagctgtgtagcagggccaacagagacaca 329
Db	69 CAGTGCACCAACCATCGAAGTGGAGTAGTAACTCACAAAGCAAGATTTGCACACCTACTCAGGATTA 128
Db	129 GTCTCAGATGTATGACCAGGACACCAACCTCGGCAAGACAGCGCTTACCAAGCTTGAGATT 188
Db	330 gtctgcgcgtcgcgggagggcacccagcccccttga-----cagctacaagcctggagct 383
Db	384 gaacttgcacccccttcacagggcaactcttcacagggcaaacacagggcctgcgaagcc 443
Db	189 GACTGTGTTCCTGCTCCCTCTGCGCACATTTTTCACAGGCAACACCGAGCCTGCAGAAGCCC 248

OY	444	tggaccacactggaaccttgccttggaagacaacaccctcgcaagccggccagaatagctcggac	503
Dd	249	TGGACCAATTGTGACTTTATCTTGGAAAGCAGACCCTCCACCCAGCCAGTAGACACTTTGGAC	308
OY	504	gcaatctgttagaagaaggaaaccccccaagccaagcagcccacagaagaccagaagccccccg	563
Dd	309	GCAGCTGTGTGAAGACAGAAGAGCTCTCTGGCGCACACTGTCTTGAGAGACCAAGCGCCCTACA	368
OY	564	gccagggcccatcacctcgttcgaagcccaactgaagccttggcccagaacctcaaggaacctcc	623
Dd	369	TTCAAGGCCAACACACACTGTTCATAATCCACACAGACTGTGGCCAGGACTTCTGAGTTGACTCT	428
OY	624	accggcccgtagaagtccccgggggcgctgagctggttcgcgcacatctcgtgagcttgagctg	683
Dd	429	GCACCCACACTTBTGTTACTTCTGTAGAGGGCCCCGTGACTTTGCTTCTCTTACAGCCCTTG----	483
OY	684	gtgctctggagctgcttgagcccccctgycacatcctctgctgccttgtacactgtctccgaaggac	743
Dd	484	--GCTGGGGCTGCTGCTGCTTGCCTTGAAGTGTGCTGTGGCCCTTGTACTCTGCTCGGAAGCT	541
OY	744	cagaggtctgcccccgatagcccaaaagcccccttgaggaggagcagtttccgaagcccccat	803
Dd	542	TGGAAATTG--CCTAACAACCTCCCAAACCTTGTGTTGGGAAACAGCTTCAGGAACCCGATT	598
OY	804	caagagagagcagcgccagcccatcaaacct	835
Dd	599	CAGGACGAACACACAGCCGACACTTACTCT	630
RESULT 14	A1323590/c		
LOCUS	A1323590	609 bp	mRNA linear EST 23-DEC-1998
DEFINITION	mp1a10.x1 Soares_rhymus_2nbmr Mus musculus cDNA clone IMAGE:573650		
	3 similar to gb:X85214.M.musculus ox40 gene (MOUSE).; mRNA sequence.		
ACCESSION	A1323590		
VERSION	A1323590.1		
KEYWORDS	EST.		
SOURCE	house mouse.		
ORGANISM	Mus musculus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
REFERENCE	1 (bases 1 to 609)		
AUTHORS	Marrin,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubque,T.,		
	Gaisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,		
	Scheilenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,		
	Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and		
	Waterston,R.		
	The WashU-HMI Mouse EST Project		
	Unpublished (1996)		
TITLE	Contact: Maria M/Mouse EST Project		
JOURNAL	WashU-HMI Mouse EST Project		
COMMENT	Washington University School of Medicine		
	4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: mouseest@wustl.edu		
	This clone is available royalty-free through LLNL ; contact the		
	IMAGE Consortium (info@image.llnl.gov) for further information.		
	MGI:348338		
FEATURES	This clone was previously sequenced on the 5' end only, this new		
	data is from the 3' end		
	High quality sequence stop: 456.		
source	Location/Qualifiers		
	1..609		

Query Match	Best Local Similarity	Matches	332: Conservative	20.3%: Score	66.7%: Pred. No.	3.4e-28: Mismatches	157: Indels	9: Gaps	2:
384	gactctgccccctgcccccccaaggagcactctctccaggcgaaacacaggcctcaagccc	443							
609	GACTGTGTTCCCTGGCCCTGCTGCGACCTTTTCTCCAGGACANNCCAGCCNTGCAAGC	550							
444	tgagccaactgcaccttgcttgaggagacacacccctgcagcgccagcaatagctcgagc	503							
549	TGNACCCNMTTGTACTATCTGAAAAAGCAGACNCCACACACCCAGTGACAGCTTGNA	490							
504	gcaatcttgaggagacagagagccccccagcagcagcccccaaggagaccagagcccccg	563							
489	GCAGCTGTGTGAGAGACAGAAAGCTCTCTGGCCACACACTGCTGTGGAGAACCCAGG	430							
564	gccagagcccatcactgtctcagcccaactggaagcctgagcccaagcctcaagagacc	623							
429	TTCAAGGCCAACACCTGTCCATCCACACACAGCTCTGGCCAGACCTTGTGAGTGTG	370							
624	accgggccccctggaaggtcccccggggcgctgagcttgcgcacactcttgagccttg	683							
369	CCACCACCTTGGTGACTCTGTAGAGGCCCCCTGCATTGCTGTTCTCTAAGCTGGGC	311							
312	--CTGGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	256							
744	cagagagctgccccccgcatgagcccaagaccctctgaggagagagcttccgcagccc	803							
255	TGGAAATTG---CTTAACACTCCCAACCTTGTGGGAAAAAGCTTGAAGGACCCCG	199							
804	caagagagagcagagccagcagcctccacccctgagcccaagatctgagccttgagcc	863							
198	CAGGAGGAACACACAGACGACACCTTACTCTGGCCAAAGATCTGAGCATTTACTAC	139							
864	ggtgagcgtgagcccg	881							
138	TGGATTATTATGGGCGACG	121							

RESULT 15

LOCUS A1914208/c 247 bp mRNA linear EST 17-DEC-1999

DEFINITION wd76t010.x1 NCI.CGAP\_Lu24 Homo sapiens cDNA clone IMAGE:2337546 3',

ACCESSION A1914208

VERSION A1914208.1 GI:5634063

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

EUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 247)

AUTHORS NCI-CGAP. <http://www.ncbi.nlm.nih.gov/ncicgap>.

TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index

/dev\_stage="4 weeks"

/lab\_host="BDH10B"

/note="Vector: pT713D-Pac (Pharmacia) with a modified polylinker. Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer (5', TGTTCACATCTGAAAGTGGAGCGGCGGCTTTTTTTTTTTTTTTTTT 3'); double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of the modified pT713 vector. RNA provided by Dr. Bertrand Jordan. Library went through two rounds of normalization, and was constructed by Bento Soares and M.Falima Bonaldo."

JOURNAL  
COMMENT

Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaabs-r@mail.nih.gov  
 Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
 Emmert-Buck, M.D., Ph.D.  
 cDNA Library Preparation: M. Bento Soares, Ph.D.  
 cDNA Library Arrayed by: Greg Lennon, Ph.D.  
 DNA Sequencing by: Washington University Genome Sequencing Center  
 Clone distribution: NCI-CGAP clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 www-bio.llnl.gov/bdrp/image/image.html  
 Insert Length: 373 Std Error: 0.00  
 Seq primer: -400P from GABCO.  
 Location/Qualifiers  
 1..247

FEATURES  
source

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 /clone="IMAGE:237536"  
 /clone\_1lb="NCI-CGAP-Lu24"  
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 /lab\_host="DH10B"  
 /note="Organ: lung; Vector: pT73D-Pac (Pharmacia) with a  
 modified polylinker; Plasmid DNA from the normalized  
 library NCI-CGAP\_Lu5 was prepared, and ss circles were  
 made in vitro. Following HAP purification, this DNA was  
 used as tracer in a subtractive hybridization reaction.  
 The driver was PCR-amplified cDNAs from a pool of 5,000  
 clones made from the same library (clonoids  
 1414920-1417991 and 1520904-1522439). Subtraction by Bento  
 Soares and M. Fatima Bonaldo."

BASE COUNT  
ORIGIN

41 a 70 c 79 g 57 t

## Query Match

19.5%: Score 206.4; DB 9; Length 247;

Best Local Similarity 96.9%: Pred. No. 9.1e-27;

Matches 221; Conservative 0; Mismatches 6; Indels 1; Gaps 1;

QY 831 accctggccaagatctgacacttgagcccaagaagtgaagctgagcccgccaagctg 890  
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 Db 247 ACCCTGGCCAGATTGTGACC-TGGGCCCCACCAAGGTGAGCTGGGCCCCGCCAGCTGG 189  
 QY 891 agcccgagaggtctgtgagcgagcaaggagtgcaagcgccctgcccgcacagctcc 950  
 |||||  
 Db 188 AGCCCGGAGGGTTGCTGGGGCAGCAGGGCAGGTGACAGCCGCTGCCGCCACAGCTCC 129  
 QY 951 tgggccaactctgacgcttctaagtgccgagtgtgctcgcgtctcttctaagtat 1010  
 |||||  
 Db 128 TGGGCCAACCTTTAGTGCCGATGGCTGCTCAGGCTCTGTGCTTACGTAT 69  
 QY 1011 gccatgatactctctgcccgcgagacacaataaaaccttgagcag 1058  
 |||||  
 Db 68 GCCATGCTACTCTCTGCCCCGCCGGGACCCCAATATAAAACCTTGGCAG 21

Search completed: June 18, 2002, 17:56:27  
 Job time: 12105 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 18, 2002, 14:34:42 ; Search time 285.57 Seconds  
(without alignments)  
6360.946 Million cell updates/sec

Title: US-09-852-845-1  
Perfect score: 1058  
Sequence: 1 cagcagagacgagatgtgc.....cacataaaacctgtgcag 1058

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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- 2: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT.\*
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- 20: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2000.DAT.\*
- 21: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT.\*
- 22: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT.\*
- 23: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.\*
- 24: /net/abs06/SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	1044.4	98.7	1057 16	AA088758 ACT-4 cell surface
2	1044.4	98.7	1057 16	AA088758 ACT-4 cell surface
3	802	75.8	1057 16	AA088758 ACT-4 cell surface
4	286.6	27.1	1317 16	AA088758 ACT-4 cell surface
5	286.6	27.1	1317 16	AA088758 ACT-4 cell surface
6	283.2	26.8	1317 16	AA088758 ACT-4 cell surface
7	283.2	26.8	1317 16	AA088758 ACT-4 cell surface
8	124.4	11.8	6080 22	AA56582 Tumour suppressor
9	111.2	10.5	117 22	AA088758 ACT-4 cell surface

C 10	111.2	10.5	117	22	AA088758	Human secondary s1
C 11	111.2	10.5	117	22	AA088758	Human secondary s1
C 12	109.4	10.3	117	22	AA088758	Oligonucleotide fo
C 13	109.4	10.3	117	22	AA088758	Human secondary s1
C 14	109.4	10.3	117	22	AA088758	Human secondary s1
C 15	108.8	10.3	6080	22	AA088758	Tumour suppressor
C 16	101.6	9.6	5148	22	AA088758	Tumour suppressor
C 17	79.8	7.5	5148	22	AA088758	Tumour suppressor
C 18	67.6	6.4	114955	20	AA088758	Human adenosine A1
C 19	59.6	5.6	114955	20	AA088758	Human adenosine A1
C 20	56	5.3	763	21	AA088758	Human molecule ass
C 21	56	5.3	813	21	AA088758	DNA encoding tumou
C 22	56	5.3	983	21	AA088758	Human tumour necro
C 23	56	5.3	983	21	AA088758	Tumour necrosis fa
C 24	56	5.3	1006	19	AA088758	Nucleotide sequenc
C 25	56	5.3	1007	21	AA088758	Human tumour necro
C 26	56	5.3	1007	21	AA088758	TR1SV1 nucleotide
C 27	56	5.3	1008	21	AA088758	Human TNF receptor
C 28	56	5.3	1008	21	AA088758	CDNA encoding huma
C 29	56	5.3	1008	21	AA088758	Human PRO364 prote
C 30	56	5.3	1008	21	AA088758	Human PRO364 CDNA
C 31	56	5.3	1008	21	AA088758	Human PRO364 prote
C 32	56	5.3	1008	22	AA088758	Native sequence of
C 33	56	5.3	1008	22	AA088758	Clone DNA47365-120
C 34	56	5.3	1008	22	AA088758	Human CDNA encodin
C 35	56	5.3	1008	22	AA088758	Human PRO364 CDNA
C 36	56	5.3	1008	22	AA088758	Human PRO364 CDNA
C 37	56	5.3	1008	22	AA088758	Human angiogenesis
C 38	56	5.3	1074	21	AA088758	Human tumour necro
C 39	56	5.3	1074	21	AA088758	TR1SV2 nucleotide
C 40	56	5.3	12425	22	AA088758	Human low density
C 41	55.2	5.2	900	21	AA088758	Monkey Fas ligand
C 42	53.4	5.0	1614	22	AA088758	Human low density
C 43	52.6	5.0	125401	22	AA088758	Streptomyces nous
C 44	52.4	5.0	3306	11	AA088758	Expressible sequen
C 45	51.6	4.9	8459	22	AA088758	Human histone deac

## ALIGNMENTS

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AC	AA088758	
XX	AA088758	
DT	21-NOV-1995	(first entry)
XX	AA088758	
DE	ACT-4 cell surface receptor CDNA sequence.	
XX	AA088758	
KW	Cell surface receptor; ACT-4; T-Lymphocyte; T-cell; Immune system;	
KW	ss.	
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OS	Homo sapiens.	
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FT	polyA_site	/*tag= b
FT	polyA_site	1042..1047
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PD	11-MAY-1995.	
XX	AA088758	
PF	03-NOV-1994;	94W0-CB02415.
XX	AA088758	
PR	03-NOV-1993;	93US-0147784.
XX	AA088758	
PA	(BECTON ) BECTON DICKINSON CO.	

PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
XX  
PI Buck DW, Engleman EG, Godfrey W;  
XX WPI: 1995-185777/24.  
DR  
DR P-PSDB: AAR/4737.  
XX  
XX  
PT Isolated ACT-4 receptor from activated T-cells - also its ligands and  
PT antibodies, useful for treating diseases of the immune system  
XX  
PS Claim 1; Fig. 5; 82pp; English.  
XX  
XX This sequence encodes the full-length cell surface receptor ACT-4  
CC isolated from activated CD4+ T-lymphocytes. The sequence may be  
CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or  
CC fragments, and antibodies may be used for the treatment of transplant  
CC rejection, graft-versus-host disease, autoimmune disease, etc.  
XX  
XO Sequence 1057 BP; 176 A; 390 C; 344 G; 147 T; 0 other;

Query Match	98.7%	Score 1044.4;	DB 16;	Length 1057;
Best Local Similarity	99.8%	Pred. No. 4.2e-181;		
Matches 1056; Conservative	0;	Mismatches 1;	Indels 1;	Gaps 1.

QY	1	caagacagagacagagaaatctgacgtgagggccctcggccgagctgggacccgctgctgacgctc	60
Db	1	caagacagagacagagaaatctgacgtgagggccctcggccgagctgggacccgctgctgacgctc	60
QY	61	tgtctctctctcgtgagccctgagggcctgagcaacgctgacgaggctccacaatgtgctcgggagacaact	120
Db	61	tgtctctctctcgtgagccctgagggcctgagcaacgctgagcaagggctccacaatgtgctcgggagacaact	120
QY	121	agcccaagagaaagaaacgggtgacctgacacagatgtgacaaggccaagagaaatgtgtagccgact	180
Db	121	agcccaagagaaagaaacgggtgacctgacacagatgtgacaaggccaagagaaatgtgtagccgact	180
QY	181	ggacgacgctcccaagaaacaaggtgtgtgcgcgtccgtgtgagggccgggctctcacacaagacgttgg	240
Db	181	ggacgacgctcccaagaaacaaggtgtgtgcgcgtccgtgtgagggccgggctctcacacaagacgttgg	240
QY	241	tcagagctccaaagccgctgcaagagccctcgacgtgtggtgttaaaccctcaagaaagtgtggagatggagag	300
Db	241	tcagagctccaaagccgctgcaagagccctcgacgtgtggtgttaaaccctcaagaaagtgtggagatggagag	300
QY	301	agacagctgtgtgacgagccacaacaagagacaagatctgtgcgctgtgcgggacgggacccacacagcccc	360
Db	301	agacagctgtgtgacgagccacaacaagagacaagatctgtgcgctgtgcgggacgggacccacacagcccc	360
QY	361	tggagcaagcttaaaagacccgtggagatgtgaactgtgccccctgtccctctcaaggagcaattcttccag	420
Db	361	tggagcaagcttaaaagacccgtggagatgtgaactgtgccccctgtccctctcaaggagcaattcttccag	420
QY	421	ggcagcaaacacagggccctgtgcaagagccctctgagacccaaactgtgcaactctgtgctgtggaagcacaaccctgtc	480
Db	421	ggcagcaaacacagggccctgtgcaagagccctctgagacccaaactgtgcaactctgtgctgtggaagcacaaccctgtc	480
QY	481	agcccggtgcagagaaataagctctcgaaagcgaatactgtgtggggagcaagagaaacccccaagcccaagc	540
Db	481	agcccggtgcagagaaataagctctcgaaagcgaatactgtgtggggagcaagagaaacccccaagcccaagc	540
QY	541	ccacagagagaaacccaagggcccccacgggccaagccacaatactgtccaaagcccaatgtgaagagccctgtgc	600
Db	541	ccacagagagaaacccaagggcccccacgggccaagccacaatactgtccaaagcccaatgtgaagagccctgtgc	600
QY	601	ccagaaacctcacaagggagacccctccaaaccgggcccgtgtgagaggttccccgggggacgtgtgacgtttg	660
Db	601	ccagaaacctcacaagggagacccctccaaaccgggcccgtgtgagaggttccccgggggacgtgtgacgtttg	660
QY	661	ccgggcaatacctctgggagccctgtgggtgtgtgtggggcgtgagccacccctgtgccaatacctctgtg	720
Db	661	ccgggcaatacctctgggagccctgtgggtgtgtgtggggcgtgagccacccctgtgccaatacctctgtg	720

Qy	721	ccctctaccctctcccgagagagacacaaagagctctgcccccgatctgcacaaagccccctgggg	780
Db	721	ccctctaccctctcccgagagagacacaaagagctctgcccccgatctgcacaaagccccctgggg	780
Qy	721	ccctctaccctctcccgagagagacacaaagagctctgcccccgatctgcacaaagccccctgggg	780
Db	721	ccctctaccctctcccgagagagacacaaagagctctgcccccgatctgcacaaagccccctgggg	780
Qy	761	gagcgagctcttcggagaccccccattccaaagagagacagagcgcagcgcacatccacatctggcca	840
Db	761	gagcgagctcttcggagaccccccattccaaagagagagacagagcgcagcgcacatccacatctggcca	840
Qy	841	agatctgaacctctgggccacacaaagcttgagacgctcgagcccccgacaaagctctggagagccggagag	900
Db	841	agatctgaac - tgggccacacaaagcttgagacgctcgagcccccgacaaagctctggagagccggagag	899
Qy	901	gtctctgctggggagacaaagggagaggtggcagggccgcctctcccgacaaagctctctctgggcaact	960
Db	900	gtctctgctggggagacaaagggagaggtggcagggccgcctctcccgacaaagctctctctgggcaact	959
Qy	961	ctgcacacgctctctctaggtctgcagatctgctctcgcgctctctctgctcttaagctatgcacatgcata	1020
Db	960	ctgcacacgctctctctaggtctgcagatctgctctcgcgctctctctgctcttaagctatgcacatgcata	1019
Qy	1021	ccctctgcccccgagagacacaaataaaanaaactctggag	1058
Db	1020	ccctctgcccccgagagacacaaataaaanaaactctggag	1057

XX	RESULT	2
XX	AA704048	
XX	AA704048 standard; CDNA; 1057 BP.	
XX	AA704048;	
XX	05-MAR-1996 (first entry)	
XX	ACT-4-h-1 receptor cDNA sequence.	
XX	ACT-4; specific binding partner. sbd; B cells; lymphocyte; GVHD.	
XX	griif versus host disease; immune response; transplantation;	
XX	autoimmune disease; inflammation; HIV; human immunodeficiency virus	
XX	HIV-1; human T lymphocyte virus; inflammatory bowel disease;	
XX	screening; identification; ss.	
XX	Homo sapiens.	
XX	Key	Location/Qualifiers
XX	CDS	15..849
XX		/*tag- a
XX	sig_peptide	/product= ACT-4-h-1 receptor.
XX		15..86
XX		/*tag- b
XX	mat_peptide	87..846
XX		/*tag- c
XX	polyA_site	1042..1048
XX		/*tag- d
XX	W09521915-A1.	
XX	17-AUG-1995.	
XX	06-FEB-1995;	95MO-GH00238.
XX	10-FEB-1994;	94US-0195967.
XX	(GREAF) GREAVES C P.	
XX	(STRD ) UNIV LEELAND STANFORD JUNIOR.	
XX	Engleman EG, Godfrey W;	
XX	WPI; 1995-293117/38.	
XX	P-PSDB; AAR79904.	
XX	Ligand, ACT-4-L, to receptor on activated CD4 positive cells	
XX	useful in treatment of various immune diseases and conditions	







QY 381 gtgtactgtgccccctgcccctccagggcactcttcccaaggcgaacacagcctgcaaf 440  
D 361 gtgtactgtgtccctctgcccctccagcactttctccaggcaaacacagcctgcaag 420  
QY 441 cccctgagcaactgtgactgtgctgggaagcacaccctgcagccgagcaatagtctg 500  
D 421 cccctgagcaactgtgactgtgctgggaagcacaccctgcagccgagcaatagtctg 480  
QY 501 gacgcactctgtggaggaaggagcccccagccagccagccgagcaataaggccccc 560  
D 481 gacgcactctgtggaggaaggagcccccagccagccagccgagcaataaggccccc 540  
QY 561 ccggccagggcccatcactgtccagcccatgaagcctgtgcccagagaactcacaggacc 620  
D 541 acattcagggcccaacacactgtccatccacacagctgtgcccagagactctgagtgccc 600  
QY 621 tcacacggcccgctggagagtcgcccgggggcgctgcggttcgcgcacatccctggcctggc 680  
D 601 tctacacccacactgtgtgagccagatcttgtgacaaaactcacacatgcccacgtgc 660  
QY 681 ctgtgtcggggcgtgcgtgcccctgtgcccctgtgcatctcctgtgcgccc 723  
D 661 ccagcactgaagcgcagggcgcgctcagcttccctctcc 703

RESULT 5

AAV32636  
ID AAV32636 standard; cDNA to mRNA; 1317 BP.  
AC AAV32636;  
XX 25-SEP-1998 (first entry)  
DT 25-SEP-1998 (first entry)  
DE OX40/Fc CDNA.  
XX OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;  
KW chimeric; ss.  
XX  
OS Synthetic.  
OS Chimeric - Homo sapiens.  
OS Chimeric - Mus sp.  
XX  
FH Key Location/Qualifiers  
FT CDS 1..1317  
FT /tag= b  
FT product= "OX40/Fc mutein"  
FT 1..618  
FT /tag= a  
FT /note= "encodes mouse OX40 extracellular domain"  
FT 619..1314  
FT /tag= b  
FT /note= "encodes mutant Fc region of human IgG1"  
FT 673..675  
FT /tag= c  
FT /note= "Changed from CTC in wild-type to GCC in  
FT mutant"  
FT 676..678  
FT /tag= d  
FT /note= "Changed from CTG in wild-type to GAG in  
FT mutant"  
FT mutation  
FT 682..684  
FT /tag= e  
FT /note= "changed from GCA in wild-type to GCG in  
FT mutant"  
XX  
PN US5783665-A.  
XX  
XX 21-JUL-1998.  
PD  
XX  
PF 22-JUN-1995; 95US-0494574.  
XX  
PR 23-JUL-1993; 93US-0097827.

PR 22-JUN-1995; 95US-0494574.  
XX  
XX (IMM V ) IMMUNEX CORP.  
XX  
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
XX WPI; 1998-427099/36.  
DR P-PSDB; AAM48976.  
XX  
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell  
PT production and binding assays for OX-40 and homologues  
PS  
PS Example 2; Col 35-38; 26pp; English.  
CC The present sequence represents the OX40/Fc cDNA which encodes a  
CC fusion protein that contains the extracellular domain of mouse OX40  
CC fused to the mutated Fc region of the human IgG1 antibody. The  
CC fusion protein was used for detecting cDNA clones encoding an OX40  
CC ligand. The invention claims for a murine OX40-L cytokine (AAM48975)  
CC that binds to the murine T cell antigen, OX40. The OX40-L protein  
CC is claimed to be useful for co-stimulation of T-cell production and  
CC in binding assays for detecting OX40 or its homologues. The OX40-L  
CC protein is also claimed to generate a TH-2 immune response.  
XX  
SO Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 27.1%; Score 286.6; DB 19; Length 1317;  
Best Local Similarity 66.6%; Pred. No. 1.5e-43;  
Matches 428; Conservative 0; Mismatches 209; Indels 6; Gaps 1;

QY 87 accgtgacggggcgtccactgtgtcggggagacactaccacagacagccggtgtgcac 146  
D 61 acagcaaggcggctcaactgtgttaactactactaccacagtggtcacaagtgctgtc 120  
QY 147 gaggtagcagcgaagcaagagtgtagcgctgcagcgctccacagacagtgctgc 206  
D 121 gaggtagcagcgaagcaagagtgtagcgctgcagcgctccacagacagtgctgc 180  
QY 207 cgtccgtgcggcgccggtcttcaacagcgctgcagctccacagcgctgcagcgctgc 266  
D 181 catccgtgtgagacactggtcttcaacagcgctgcagctccacagcgctgcagcgctgc 240  
QY 267 agctgtgttaacctagaagtgtagtgagcgaagcagctgtgcacggtccacagagac 326  
D 241 acacagtgtaacacatcgaagtgtagtgagcagcagcagtgtaacacagtgtaacac 300  
QY 327 acagtcgcgcgttcgcggcggtgcacccacagcccttga-----cagctacaagccttga 380  
D 301 actgtctgagatgtagaccagagcaccacactgcgagcagcagcgtctacagcttga 360  
QY 381 gtgtactgtgccccctgcccctccagggcactcttcccaaggcgaacacagcctgcaaf 440  
D 361 gtgtactgtgtccctctgcccctccagcactttctccaggcaaacacagcctgcaag 420  
QY 441 cccctgagcaactgtgactgtgctgggaagcacaccctgcagccgagcaatagtctg 500  
D 421 cccctgagcaactgtgactgtgctgggaagcacaccctgcagccgagcaatagtctg 480  
QY 501 gacgcactctgtggaggaaggagcccccagccagccagccgagcaataaggccccc 560  
D 481 gacgcactctgtggaggaaggagcccccagccagccagccgagcaataaggccccc 540  
QY 561 ccggccagggcccatcactgtccagcccatgaagcctgtgcccagagaactcacaggacc 620  
D 541 acattcagggcccaacacactgtccatccacacagctgtgcccagagactctgagtgccc 600  
QY 621 tcacacggcccgctggagagtcgcccgggggcgctgcggttcgcgcacatccctggcctggc 680  
D 601 tctacacccacactgtgtgagccagatcttgtgacaaaactcacacatgcccacgtgc 660  
QY 681 ctgtgtcggggcgtgcgtgcccctgtgcccctgtgcatctcctgtgcgccc 723

Db 661 ccagcactgaagccgagggcgccgctcagctctctctcc 703

RESULT 6  
AA00826  
ID AAT00826 standard; CDNA to mRNA; 618 BP.  
AC AAT00826;  
XX  
XX 30-MAR-1996 (first entry)  
XX  
XX Mouse type-II membrane polypeptide OX40 extracellular domain.  
DE  
XX OX40; OX40-L; cytokine; cell surface molecule;  
KM membrane glycoprotein; ss.  
XX  
XX Mus musculus.  
OS  
XX US5457035-A.  
PN  
XX 10-OCT-1995.  
PD  
XX 23-JUL-1993; 93US-0097827.  
PF  
XX 23-JUL-1993; 93US-0097827.  
PR  
XX 23-JUL-1993; 93US-0097827.  
PA (IMMV ) IMMUNEX CORP.  
XX  
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
XX WPI: 1995-357992/46.  
DR P-PSDB; AAR81881.  
XX  
XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors  
PT and host cells, used to produce recombinant ligand used in e.g.  
PT prim. T cell culture, to modulate immune response etc.  
XX  
XX Example 1; Column 31-32; 26pp; English.  
PS  
XX This sequence encodes the extracellular domain of OX40, a membrane  
CC glycoprotein present on the CD4 positive subset of activated T  
CC cells.  
XX  
XX Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;

Query Match 26.8%; Score 283.2; DB 16; Length 618;  
Best Local Similarity 70.6%; Pred. NO. 6.4e-43;  
Matches 394; Conservative 0; Mismatches 158; Indels 6; Gaps 1;

QY 87 accgtagcggtctcactgtgtcggtgagacacacccacgaagcagcggtgtgtcac 146  
DB 61 acagacagcggtcactgtgttaaacataccacccaggtgtcagtgctgtcgt 120  
QY 147 gagtcagggccagcagcagggatgtgtgagccgctgacagcggtcccaagaacgggtgtgc 206  
DB 121 gagtcagggccagcagcagggatgtgtgagccgctgacacacagggatctctatgt 180  
QY 207 cgtccgtgcggcggtgtcttacaacgagtggtcagctcccaagcgtgtcaagccctgtc 266  
DB 181 catccgtgtgagactgtgtcttacaatgaagctgtcgaattgatctacccgaagcagtg 240  
QY 267 acgtgtgttaacctagaagtggtgagtgagcggagcagcgtgtgtgacagccacaagac 326  
DB 241 acacagtgtaacacatcgaagtgtgaagtgaactcaagcagaattgtcacctactcagat 300  
QY 327 acagctcgcgtgtgcggcgccagccacccctgtga-----cagctacaagccttga 380  
DB 301 actgtctcagatcagacacagccacacacccaccccgagcagcgtcaccaagcttga 360  
QY 381 gttgactgtgccccctcctccacagagcactcttccagcagcagaacagcgtgtcaag 440  
DB 361 gttgactgtgtctccctcctcctcgtgcacacttctcagcagaacacacagcgtgtcaag 420

QY 441 cccgtgaccacatgcaccttggctgtggaagcacacccctgtcagccggccagcaatagtctg 500  
DB 421 cccgtgaccacatgtactcttactgtgaagcagaccccgccacccagcagtgacagcttg 480  
QY 501 gacgcacatctgtgagcagcagggagccccccagcagcagcagccacagagagccccc 560  
DB 481 gacgcagctctgtgagcagcagcagcagcagcagcagcagcagcagcagcagcagc 540  
QY 561 ccggccagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 620  
DB 541 acattcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 600  
QY 621 tccaccggccgctgtgag 638  
DB 601 tctacaccacactgtgtg 618

RESULT 7  
AAV32640  
ID AAV32640 standard; CDNA to mRNA; 618 BP.  
XX  
XX AAV32640;  
AC  
XX 25-SEP-1998 (first entry)  
XX  
XX Mouse OX40 extracellular domain encoding CDNA.  
DE  
XX OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;  
KM OX40/Fc; ss.  
XX  
XX Mus sp.  
OS  
XX  
XX Key Location/Qualifiers  
FH 1. 618  
FT CDS  
FT  
FT /product= "Mouse OX40 extracellular region"  
FT /note= "CDS does not contain a stop codon"

US5783665-A.  
21-JUL-1998.  
22-JUN-1995; 95US-0494574.  
23-JUL-1993; 93US-0097827.  
PR 22-JUN-1995; 95US-0494574.  
XX  
XX (IMMV ) IMMUNEX CORP.  
XX  
XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
XX WPI: 1998-427099/36.  
DR P-PSDB; AAW48977.  
XX  
XX Purified polypeptide OX-40 ligands - for co-stimulation of T-cell  
PT production and binding assays for OX-40 and homologues  
XX  
XX Example 1; Col 31-32; 26pp; English.  
PS  
XX The present sequence represents the mouse OX40 extracellular domain  
XX encoding CDNA. The extracellular domain of OX40 is its ligand  
CC binding domain. The present CDNA was used in the construction of the  
CC chimeric OX40/Fc CDNA (AAV32640). The invention claims for a murine  
CC OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen.  
CC The OX40-L protein is claimed to be useful for co-stimulation of  
CC T-cell production and in binding assays for detecting OX40 or its  
CC homologues. The OX40-L protein is also claimed to generate a TH-2  
XX immune response.  
XX  
XX Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;

Query Match	26.8%;	Score 283.2;	DB 19;	Length 618;
Best Local Similarity	-70.6%;	Pred. No. 6.4e-43;		
Matches 39%;	Conservative	0;	Mismatches 158;	Indels 6;
				Gaps 1;

QY	87	acccgtgcaggcggtcccaactctgttcgcggggaacactaccacgaagacggcggtcccaac	146
Db	61	acacgaagcgagcggtctcaactctgtttaacaatacctaccacccgaagtgttacaagatgctctgt	120
QY	147	gaagtgcagcgccaggaacaaaggatagtgtagcgcgtctgcagccgcgtctcccaagaacagtgtagc	206
Db	121	gagtgccagcgccagggccatgtagtgtagaacgcgtgtgatatcataccagggatgatactatgt	180
QY	207	cgtccgtgcggggccggggtctctacaacagacgtgtgaagcttccaagccgtgtcaagccctgc	266
Db	181	catccgcgtgtgaagactggtctcttacaatgaagcgtgtcaattatgatacctgcgaagcagtgat	240
QY	267	acgtgtggtgatacctcaacaaatgtggaggtgtgaagcggaaagcagctgtgcacgcgcgaacagac	326
Db	241	acacacagtcgaacacctcgaagaatgtgaagaatcagaagaatgtgacaaactactaccagat	300
QY	327	acagatctccgcgcgtgcgcggcgagcgacccacgaacccctctgga-----cagctacaagctctgga	380
Db	301	actgtctgcagatgttagaaccagacacccaacctctcggagaagaaacggctacaaagcttggaa	360
QY	381	gttgactgtgtcccccgtgccttccagggactcttctcccaaggcgaacaacagagccttgcgaag	440
Db	361	gttgactgtgttccctctgcctcctcctgcgcacattcttcccaaggacaacaacagagccttgcgaag	420
QY	441	ccccgtgcgaacatgcacactctggtcggggaagaacacacccctgtgaagccgcggccacaataaactgc	500
Db	421	ccccgtgcgaacatgtataccttatactcgggaagaagaccggccacacccaacgaacatgtgacaacttgc	480
QY	501	gaagcaatactgttagggagcaaggagacccccccacgacgaagcaccgaaggagacccaagggtccccc	560
Db	481	gaagcagatctgttagggagcaaggagacgtctctgtgcacaactgtctctggtgagaccacagcgccct	540
QY	561	ccggcagagcggccatcaactgtcttcagcccaactgaaagcctgtgcgcgaagaacctacaaggagacc	620
Db	541	acatttcagcgccaacacactgtctacaatacacaacacacagctgtgcgcagagacttctgagtgtccc	600
QY	621	tcgaacccggcccgctgtgag	638
Db	601	tctaacaccacacttgcgtg	618

RESULT	8
AAAS46582/C	
ID	AAAS46582 standard; DNA; 6080 BP.
XX	
AC	AAAS46582;
XX	
DT	18-DEC-2001 (first entry)
XX	
DE	Tumour suppressor gene derived chemically modified sequence #304.
XX	
KW	Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW	cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP
KW	cytosine methylation; ds.
XX	
OS	Homo sapiens.
XX	
PN	W0200168912-A2.
XX	
PD	20-SEP-2001.
XX	
PE	15-MAR-2001; 2001MO-EP02955.
XX	
PR	15-MAR-2000; 2000DE-1013847.
PR	06-APR-2000; 2000DE-1019058.
PR	07-APR-2000; 2000DE-1019173.
PR	30-JUN-2000; 2000DE-1032529.
PR	01-SEP-2000; 2000DE-1043826.
XX	

PA (EPiG-) EPIGENOMICS AG.  
XX  
PI Olek A, Piepenbrock C, Berlin K;  
XX  
DR WPI; 2001-602752/68.  
XX  
XX Fragments of chemically modified genes associated with tumour suppressor  
PT genes and oncogenes, useful in designing primers and probes for  
PT analysing diseases associated with cytosine methylation state e.g.  
PT cancer  
XX  
PS Claim 1; SEQ ID No 304; 27pp; English.

The invention relates to a nucleic acid comprising a sequence of 18 bases, of a segment of chemically pretreated DNA (cp DNA) e.g. with bisulphite, of genes associated with tumour suppression and oncogenes having a sequence taken from 536 (actually 533 since numbers 408, 458 and 500 are missing from the sequence listing) sequence (5s) and sequences complementary to (5s). The nucleic acid may be a peptide nucleic acid-oligonmer (PNA) of at least 9 nucleotides and may form part of a set of probes for detecting the cytosine methylation status and/or single nucleotide polymorphisms and also to be used in an array for analysing diseases associated with CpG dinucleotides e.g. cancers and tumours. The probes can also be used in a method for ascertaining genetic and/or epigenetic parameters for the diagnosis and/or therapy of existing diseases or the predisposition to specific diseases, by analysing cytosine methylations. The parameters may be compared to another set of genetic and/or epigenetic parameters, the differences serving as basis for diagnosis and/or prognosis events which are disadvantageous to patients. The present sequence is one of the 533 genomic sequences derived from tumour suppressor genes and oncogenes. Sequences with even numbered Seq ID numbers are the complementary sequence of the corresponding odd numbered sequence (e.g. ID 2 and ID1, ID 536 and ID 535, except for those whose partner sequence is missing).  
 Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at [http://wipo.int/pub/published\\_pct\\_sequences](http://wipo.int/pub/published_pct_sequences).

Sequence 6080 BP; 1124 A; 278 C; 1963 G; 2715 T; 0 other;

Query Match	11.8%	Score 124.4	DB 22	Length 6080
Best Local Similarity	74.8%	Pred. No. 4.3e-14		
Matches 169, Conservative	0	Mismatches 56	Indels 1	Gaps 1

OY	832	ccggcgccaagatcttgacaccttgccaccacaagtgtagcgcctggcgccggccaagctcga	891
Db	6080	cccttaccaccaaatattataac--ttaaaccaccacaaatataagcgttaaaccccgcccaactaaa	6022
OY	892	gcccgaagtgctcgtcgtggcgagcagggcaggtgcacgcgcgcctgcgcgcgaacgctct	951
Db	6021	accgcaaaaatcttacttaacgacacaaacaaatracaaaccgccttaccgccgacgcctct	5962
OY	952	gggcgaactctgcacgcltcctaggtgcgaatggctgcctccgcgctctcgtcttactgata	1011
Db	5961	aaaccaactctacaccccttctaaataccgatactacgtccgcactcttacttactgagtata	5902
OY	1012	ccatgcatcactctctgcgcggcgaggaccacaataataaaacttggca	1057
Db	5901	ccatpatactcttaccgccggaacacaaatataaaaccttataca	5856

RESULT 9  
 AAH24887/C  
 ID AAH24887 standard; DNA; 117 bp.  
 XX  
 AC AAH24887;  
 XX  
 DT 22-AUG-2001 (first entry)  
 XX  
 DE Oligonucleotide for a secondary signalling motif

```
XX stimulatory primary signalling motif; immune cell; signal transduction;
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;
KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;
KW dermatological disease; psoriasis; neurological disease;
KW multiple sclerosis; transplant-related disease; metabolic disease;
KW organ transplant rejection; graft versus host disease;
KW idiopathic disease; diabetes; cancer; ss.
XX Synthetic.
OS
XX WO200132709-A2.
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-GB04183.
XX
XX 01-NOV-1999; 99GB-0025848.
XX
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX
XX Finney HM, Lawson ADG;
XX
XX WPI; 2001-389718/41.
XX
XX Novel cytoplasmic signalling protein and chimeric receptor protein,
XX useful for treating HIV infection, asthma, eczema, psoriasis, multiple
XX sclerosis, contain non-natural stimulatory primary signalling motif -
XX
XX Example 2; Fig 3; 45pp; English.
XX
XX Oligonucleotides AAH24486-87 were used to construct DNA encoding
XX secondary signalling sequences. The specification describes stimulatory
XX primary signalling motifs. Primary motifs are efficient at at
XX mediating immune cell signal transduction, particularly when
XX incorporated in an intracellular signalling domain of a chimeric
XX receptor. The primary signalling motif can be combined in any way so
XX as to achieve the desired level of activation (or inhibition) of a
XX number of secondary messenger cascades. The signalling motifs are useful
XX in therapy and in the manufacture of medicament for treating or
XX preventing disease in humans or animals. They are are useful for treating
XX human patients suffering from infectious diseases e.g. human
XX immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
XX such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
XX sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
XX diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
XX transplant rejection, graft versus host disease, metabolic/idiopathic
XX disease e.g. diabetes, and cancer.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
SO
Query Match 10.5%; Score 111.2; DB 22; Length 117;
Best Local Similarity 97.4%; Pred. No. 1.1e-11;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 735 cggaggagaccagagctgcgcccgatgccacaagccccctgtggggagagcagtttcgg 794
DB 116 CGAGGAGACCAAGAGCTGCCCCCGCATGCCCAAAACCCCTGGGGAGAGCAGTTTCCCG 57
QY 795 acccccatcagaagagagcagagcgagccgacctccacctgtggccaagatcgacc 850
DB 56 ACCCCCATCAAGAGAGAGGAGCGCCGACGCTCCACCTCGGCCCAAGATCGGATC 1
RESULT 10
AAH24478/C
ID AAH24478 standard; DNA; 117 BP.
XX AAH24478;
XX
XX 07-AUG-2001 (first entry)
XX
```

```
DE Human secondary signalling motif SB34 oligo F1340B.
XX
XX Human: primary signalling motif; sequence block; SB; immunosuppressive;
KW secondary signalling sequence; antimicrobial; antiinflammatory;
KW dermatological; neuroprotective; cytostatic; anti-HIV; antistimatic;
KW antistickling; antipsoriatic; antidiabetic; gene therapy; diabetes;
KW immune cell signal transduction; infection; inflammation; cancer;
KW autoimmune disease; congenital disease; psoriasis; neurological disease;
KW organ transplant rejection; ss.
XX
XX Homo sapiens.
OS
XX WO200132867-A1.
XX 10-MAY-2001.
XX
XX 01-NOV-2000; 2000WO-GB04193.
XX
XX 01-NOV-1999; 99GB-0025853.
XX
XX (CELL-) CELLTech CHIROSCIENCE LTD.
XX
XX Finney HM, Lawson ADG;
XX
XX WPI; 2001-328791/34.
XX
XX New nucleic acids encoding polypeptides with expanded primary signalling
XX motifs, for use in gene therapy, particularly for treating or
XX preventing infections, inflammations or autoimmune diseases in humans
XX
XX Example 2; Fig 3; 43pp; English.
XX
XX The invention relates to novel primary signalling motifs containing
XX a consensus amino acid sequence. These motifs are extremely
XX efficient at mediating immune cell signal transduction, particularly
XX when incorporated into an intracellular signalling domain of a chimeric
XX receptor. Nucleic acids that encode, and polypeptides that contain,
XX these primary signalling motifs are useful in medicine and research.
XX They are useful in therapy, or in the manufacture of a medicament for
XX treating or preventing disease in humans or in animals. These diseases
XX include infections (e.g. HIV (human immunodeficiency virus) infection),
XX inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital
XX diseases (e.g. cystic fibrosis or sickle cell anemia), dermatological
XX diseases (e.g. psoriasis), neurological diseases (e.g. multiple
XX sclerosis), organ transplant rejection or graft-versus-host disease, or
XX metabolic/idiopathic diseases (e.g. diabetes or cancer). The
XX present sequence is one of a large number of oligonucleotides used in
XX the construction of sequence blocks (SBS) of primary and secondary
XX signalling motifs. Primary signalling motifs are sequences that
XX transduce either a stimulatory or an inhibitory signal, which regulates
XX primary activation of the T cell receptor (TCR) complex. Secondary
XX motifs impart secondary or co-stimulatory signalling capacity to a
XX molecule in T cells.
XX
XX Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
SO
Query Match 10.5%; Score 111.2; DB 22; Length 117;
Best Local Similarity 97.4%; Pred. No. 1.1e-11;
Matches 113; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 735 cggaggagaccagagctgcgcccgatgccacaagccccctgtggggagagcagtttcgg 794
DB 116 CGAGGAGACCAAGAGCTGCCCCCGCATGCCCAAAACCCCTGGGGAGAGCAGTTTCCCG 57
QY 795 acccccatcagaagagagcagagcgagccgacctccacctgtggccaagatcgacc 850
DB 56 ACCCCCATCAAGAGAGAGGAGCGCCGACGCTCCACCTCGGCCCAAGATCGGATC 1
RESULT 11
AAH24544/C
```

ID	AAH24544 standard; DNA; 117 BP.
XX	
AC	AAH24544;
XX	
DT	08-AUG-2001 (first entry)
XX	
DE	Human secondary signalling motif SB34 oligo F1340B.
XX	
KW	Human; anti-HIV; antiinflammatory; antiasthmatic; dermatological;
KW	antislackling; antiproliferatic; neuroprotective; immunosuppressive;
KW	antidiabetic; cyrostatic; HIV infection; inflammation;
KW	autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;
KW	neurological disease; organ transplant rejection; diabetes; cancer;
KW	graft-versus-host disease; adaptor receptor protein; sequence block;
XX	SB; primary signalling motif; secondary signalling motif; ss.
OS	
XX	Homo sapiens.
XX	
PN	WO200132866-A2.
XX	
PD	10-MAY-2001.
XX	
PF	01-NOV-2000; 2000WO-GB04189.
XX	
PR	01-NOV-1999; 99GB-0025854.
XX	
PA	(CELL-) CELLTECH CHIROSCIENCE LTD.
XX	
PI	Finney HM, Lawson ADG;
XX	
DR	WPI; 2001-328790/34.
XX	
PT	Novel polynucleotide encoding adaptor receptor protein useful for
PT	treating human immunodeficiency virus (HIV) infection, asthma, cystic
PT	fibrosis, multiple sclerosis, organ transplant rejection, diabetes and
XX	cancer
PS	
XX	Example 3; Fig 3; 52pp; English.
CC	
CC	The invention relates to a novel nucleic acid encoding an adaptor
CC	receptor protein comprising an extracellular ligand-binding domain, a
CC	transmembrane domain and an intracellular signalling domain. The
CC	intracellular signalling domain comprises the cytoplasmic portion of at
CC	least one adaptor protein, and the extracellular ligand-binding domain
CC	is not CDR or a major histocompatibility complex (MHC) class I protein.
CC	The adaptor receptor protein and the nucleic acid encoding it are useful
CC	in therapy. They are useful in the manufacture of a medicament for the
CC	treatment or prevention of disease in humans and animals. They are useful
CC	in the treatment of infectious diseases (e.g. HIV infection),
CC	inflammatory and autoimmune diseases (e.g. asthma and eczema),
CC	congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),
CC	dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)
CC	multiple sclerosis), organ transplant rejection, graft-versus-host
CC	disease and metabolic/idiopathic diseases such as diabetes and cancer.
CC	The present sequence is one of a large number of oligonucleotides used
CC	in the construction of sequence blocks (SBS) of primary and secondary
CC	signalling motifs. Primary signalling motifs transduce either a
CC	stimulatory or an inhibitory signal, which regulates primary activation
CC	of the T cell receptor (TCR) complex. Secondary signalling motifs impart
CC	secondary or co-stimulatory signalling capacity to a molecule in T
CC	cells. Primary and secondary signalling motifs may be used as
CC	components of the adaptor receptor protein of the invention.
XX	
XX	Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;

	Query Match	10.5%	Score 111.2;	DB: 22;	Length 117;
	Best Local Similarity	97.4%;	Pred. No. 1.le-11;		
	Matches 113;	Conservative	0;	Mismatches 3;	Indels 0;
					Gaps 0;
QY	735	cggaggacacgaagctgtccccgcgattgcacccaacagcccccctgtggggagagcagtttcg	794		
b	116	cgagagggacacgaagcgtccccccatcccccaaaagccccctggggagagcagtttcg	57		

**RESULT 12**

AH2486  
AH2486 standard; DNA; 117 BP.

AH2486;  
22-AUG-2001 (first entry)

Oligonucleotide for a secondary signalling motif.

Stimulatory primary signalling motifs: immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; idiopathic disease; diabetes; cancer; ss.

Synthetic.  
WO200132709-A2.  
10-MAY-2001.  
01-NOV-2000; 2000MO-GB04183.  
01-NOV-1999; 99GB-0025848.  
(CELL-) CELLTECH CHIROSCIENCE LTD.  
Finney HM, Lawson ADG;  
WPI; 2001-389718/41.

Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -

Example 2; Fig 3; 45pp; English.

Oligonucleotides AH2486-87 were used to construct DNA encoding secondary signalling sequences. The specification describes stimulatory primary signalling motifs. Primary motifs are efficient at at mediating immune cell signal transduction, particularly when incorporated in an intracellular signalling domain of a chimeric receptor. The primary signalling motif can be combined in any way so as to achieve the desired level of activation (or inhibition) of a number of secondary messenger cascades. The signalling motifs are useful in therapy and in the manufacture of medicament for treating or preventing disease in humans or animals. They are useful for treating human patients suffering from infectious diseases e.g. human immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases such as asthma and eczema, congenital diseases e.g. cystic fibrosis, sickle cell anemia, dermatological diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis, transplant-related disease e.g. organ transplant rejection, graft versus host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.

Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

	Query Match	10.38;	Score 109.4;	DB 22;	Length 117;
	Best Local Similarity	99.1%;	Pred. No. 2.3e-11;		
	Matches 110;	Conservative	0;	Mismatches 1;	Indels 0;
07	cggagagacacagagctgcctcccgatgcccacaagccccctggggagagcagtttcgg 794				





CC of the T cell receptor (TCR) complex. Secondary signalling motifs impart  
CC secondary or co-stimulatory signalling capacity to a molecule in T  
CC cells. Primary and secondary signalling motifs may be used as  
CC components of the adaptor receptor protein of the invention.  
XX Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;

Query Match 10.3%; Score 109.4; DB 22; Length 117;  
Best Local Similarity 99.1%; Pred. No. 2.3e-11;  
Matches 110; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 735 cgaagagaccagagctgcccccgatgcccacaagccccctggggagagcagttccgg 794  
|||||  
Db 6 cgaagagaccagagctgcccccgatgcccacaagccccctggggagagcagttccgg 65

QY 795 accccatccaaagagagcagcgccagccaccctcaccctggccaagatc 845  
|||||  
Db 66 accccatccaaagagagcagcgccagccaccctcaccctggccaagatc 116

RESULT 15  
AAS46581  
ID AAS46581 standard; DNA; 6080 BP.

XX AAS46581;

DT 18-DEC-2001 (first entry)

DE Tumour suppressor gene derived chemically modified sequence #303.

XX Human; tumour suppressor gene; oncogene; antitumour; cytostatic;  
KW cancer; tumour; Cpg dinucleotide; single-nucleotide polymorphism; SNP;  
XX cytosine methylation; ds.

OS Homo sapiens.

XX WO200168912-A2.

XX 20-SEP-2001.

XX 15-MAR-2001; 2001WO-EP02955.

XX 15-MAR-2000; 2000DE-1013847.

XX 06-APR-2000; 2000DE-1019058.

XX 07-APR-2000; 2000DE-1019173.

XX 30-JUN-2000; 2000DE-1032529.

XX 01-SEP-2000; 2000DE-1043826.

XX (EPIC-) EPIGENOMICS AG.

XX Olek A, Piepenbrock C, Berlin K;

XX WPI; 2001-602752/68.

XX Claim 1; SEQ ID NO 303; 27pp; English.

XX The invention relates to a nucleic acid comprising a sequence of 18

XX bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with

XX bisulphite, of genes associated with tumour suppression and

XX oncogenes having a sequence taken from 536 (actually 533 since

XX numbers 408, 458 and 500 are missing from the sequence listing) sequences

XX (Ss) and sequences complementary to (Ss). The nucleic acid may be a

XX peptide nucleic acid-oligomer (PNA) of at least 9 nucleotides and may

XX form part of a set of probes for detecting the cytosine methylation state

XX and/or single nucleotide polymorphisms and also to be used in an

XX array for analysing diseases associated with Cpg dinucleotides e.g.

XX cancers and tumours. The probes can also be used in a method for

CC ascertaining genetic and/or epigenetic parameters for the diagnosis  
CC and/or therapy of existing diseases or the predisposition to specific  
CC diseases, by analysing cytosine methylations. The parameters may be  
CC compared to another set of genetic and/or epigenetic parameters, the  
CC differences serving as basis for diagnosis and/or prognosis events which  
CC are disadvantageous to patients. The present sequence is one of the  
CC 533 genomic sequences derived from tumour suppressor genes and  
CC oncogenes.

CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.

XX Sequence 6080 BP; 1015 A; 278 C; 1978 G; 2809 T; 0 other;

Query Match 10.3%; Score 108.8; DB 22; Length 6080;  
Best Local Similarity 70.2%; Pred. No. 2.9e-11;  
Matches 146; Conservative 0; Mismatches 62; Indels 0; Gaps 0;

QY 851 ttggcccccacaggtgacgctggccccgcagagctggaagcccgaggggtctgtgg 910  
|||||

Db 19 ttgggttatttaagtgagcgttgggttctgttaagttggagttcgaggggtttgtgg 78

QY 911 cgaagagagcaggtgcagggccgctgccccgcagcgtctctggccaactctgcacglt 970  
|||||

Db 79 cgaagagagcaggtgcagggccgctgccccgcagcgtctctggccaactctgtatcgtt 138

QY 971 ctaggctccgagtgctgctcgcgctctcgtctacgtatgcacatcactctctgcc 1030  
|||||

Db 139 ttaggtgtcagtgatgtgttctggttttctttagctatgtatgtatattttgttt 198

QY 1031 cgcgggaccacaataaaaccttggcag 1058  
|||||

Db 199 cgcgggattataataaaatttggtag 226

Search completed: June 18, 2002, 18:50:45  
Job time: 15363 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:15:24 ; Search time 1824.31 Seconds  
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Scoring table: OLIGO NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1797656 seqs, 10463268293 residues

Word size : 0

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Minimum DB seq length: 0

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Post-processing: Listing first 50 summaries

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4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vi:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vi:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Query	Score	Match	Length	DB	ID	Description
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1	886	83.7	1057	6	AR048669	AR048669 Sequence
2	886	83.7	1057	6	AR156875	AR156875 Sequence
3	831	78.5	1034	9	S76792	S76792 OX40-cell s
4	740	69.9	1373	9	HSROX40MR	X75962 H. sapiens m
5	207	19.6	5150	9	HSR277151	X1277151 Homo sapi
6	207	19.6	11119	2	AL162741	AL162741 Homo sapi
7	207	19.6	210944	2	AL1390719	AL1390719 Homo sapi
8	83	7.8	117	6	AX134865	AX134865 Sequence
9	83	7.8	117	6	AX134962	AX134962 Sequence
10	83	7.8	117	6	AX135075	AX135075 Sequence
11	78	7.4	117	6	AX134866	AX134866 Sequence
12	78	7.4	117	6	AX134963	AX134963 Sequence
13	78	7.4	117	6	AX135076	AX135076 Sequence
14	32	3.0	1373	9	HSROX40MR	X75962 H. sapiens m
15	28	2.6	618	6	AR019518	AR019518 Sequence
16	28	2.6	618	6	114933	114933 Sequence
17	28	2.6	883	10	MMOX40	221674 M. musculus
18	28	2.6	1317	6	AR019521	AR019521 Sequence
19	28	2.6	1317	6	114936	114936 Sequence
20	28	2.6	2907	10	MMDNAOX40	X85214 M. musculus
21	28	2.6	60953	2	AC100470	AC100470 Mus muscu
22	28	2.6	253111	2	AF627204	AF627204 Mus muscu
23	28	2.6	254197	2	AF389853	AF389853 Mus muscu
24	23	2.2	5148	6	AX251339	AX251339 Sequence
25	23	2.2	104480	2	AC007905	AC007905 Homo sapi
26	21	2.0	877	4	AB003911	AB003911 Rabbit mr
27	21	2.0	1420	9	BC002494	BC002494 Homo sapi
28	21	2.0	1569	6	AX202231	AX202231 Sequence
29	21	2.0	1632	9	HSR802071	AL137382 Homo sapi
30	21	2.0	1634	9	BC021574	BC021574 Homo sapi
31	21	2.0	4656	4	SSPROPLAU	X92447 S. scrofa pr
32	21	2.0	4657	4	SSY11872	Y11872 S. scrofa up
33	34	2.0	38640	1	SCL2	AL137778 Streptomy
34	21	2.0	120766	9	AC004150	AC004150 Homo sapi
35	21	2.0	139999	8	AC018727	AC018727 Oryza sat
36	21	2.0	175799	2	AC026583	AC026583 Homo sapi
37	21	2.0	184476	2	AC009113	AC009113 Homo sapi
38	21	2.0	185243	2	AC021958	AC021958 Homo sapi
39	21	2.0	189150	2	AL603804	AL603804 Mus muscu
40	21	2.0	200882	2	AL591181	AL591181 Homo sapi
41	21	2.0	202668	2	AC009715	AC009715 Homo sapi
42	21	2.0	214180	2	AL360082	AL360082 Homo sapi
43	21	2.0	218598	2	AC023855	AC023855 Homo sapi
44	21	2.0	300000	9	AL645813	AL645813 Human DNA
45	20	1.9	291	4	BOVBTB13	D90132 Bovine mRNA
46	20	1.9	1017	10	RSOX40	X17037 Rat mRNA fo
47	20	1.9	1995	10	MMU294749	AT294749 Mus muscu
48	20	1.9	10309	1	AE003929	AE003929 Xylella f
49	20	1.9	12249	1	AE004632	AE004632 Pseudomon
50	20	1.9	26809	1	SC3A4	AL354616 Streptomy

## ALIGNMENTS

RESULT 1

AR048669

LOCUS AR048669 1057 bp DNA

DEFINITION Sequence 1 from patent US 5821332.

ACCESSION AR048669

VERSION AR048669.1 GI:5971012

KEYWORDS

SOURCE

ORGANISM

Unknown.

REFERENCE 1 (bases 1 to 1057)

AUTHORS Godfrey,W., Buck,D. and Engleman,E.G.

TITLE Receptor on the surface of activated CD4.sup.+ T-cells: ACT-4

JOURNAL Patent: US 5821332-A 1 13-OCT-1998;

FEATURES

source

1. 1057

/organism="unknown"

BASE COUNT 176 a 390 c 344 g 147 t





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DEFINITION	H.sapiens mRNA for OX40 homologue.		
ACCESSION	X75962		
VERSION	X75962.1	GI:472957	
KEYWORDS	OX40 antigen.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Humayori, Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Latza, U., Durkop, H., Schnitger, S., Ringeling, J., Eitelbach, F., Hummel, M., Fenske, C. and Stein, H.		
TITLE	The human OX40 homologue: cDNA structure, expression and chromosomal assignment of the ACT35 antigen		
JOURNAL	Eur. J. Immunol. 24 (3), 677-683 (1994)		
REFERENCE	94170844		
AUTHORS	Latza, U.		
TITLE	Direct Submission		
JOURNAL	Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz, Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG		
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	QDYRCRCRAGTQPLDYSKPGVCAPCPGHSPGDNQACKPMTCTAGKHTLQIPASN		
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	814. .958		
	repeat_region		
	959. .1079		
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	1341. .1346		
	polya_site		
	1358		
BASE COUNT	257 a 452 c 423 g 241 t		
ORIGIN			
Query Match	69.9% Score 740; DB 9; Length 1373;		
Best Local Similarity	99.8% Pred. No. 0;		
Matches 840; Conservative	0; Mismatches 2; Indels 0; Gaps 0;		
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Db	1	CGAGGATGTGCTGGGGGCTGGCGGGCTGGCGGGCCGCGGCTGCTGCTGCTCTCC	60
QY	70	tgagcctgagcgctgagcagctgaacgggctccacatgctgcggaggaacaccacccagca	129
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QY	130	acgacggctgctgcacacagctgacagcgccagggcaacaggagatggtgagccgctgcagcgct	189
Db	121	ACGACCGGCTGCTGCACAGATGACAGCCAGGCAACGGGATGAGTGAACCGCGTCAACGCGCT	180
QY	190	ccaggaacaggtgtgacgctccgttgaggccggagctctacacgaagtgtagcagctca	249

Dd	181	CCCAACAACGGGTGTGCGCTGCCGTCCGTCCGGCCGGGGCTTCTACAAGCAGCTGTTCAGCTCCA	240
Oy	250	aagcgtgcaagccctgcacgcttgatgtaacctagaagtggagttgacggaaacgaactgt	309
Dd	241	AGCCGTGCAGAGCCCTTGACAGTGGTGTAACTCAGAAGTGGAGTGAAGCGAAGCACACTTT	300
Oy	310	gcaagcgcaacaaggacacagtcctgcgcgtgcggagcgagcaaccagcccttgcagact	369
Dd	301	GCACGCGCCACACAGAACAGTCTGCCTGCGCGGGCGGGACCCAGGCCCTTGACAGCT	360
Oy	370	aaaagcctggagttgactgtgccccctgcgccctccagggagactctctcccagcgataaac	429
Dd	361	ACAACCCTGGAATTACTGTGTGCCCTGCTCCCTGCATCCAGGGCATTTCTCCACGGCCGACAAAC	420
Oy	430	aagcctgcgaagccctgcgacccaactgacacttgctgcgtggaagcacacacccctgcagcgcca	489
Dd	421	AGGCTGCAGAGCCCTTGACCAACTGCACTTGGCTTGGAAGACACACCTTGCAAGCGGCCA	480
Oy	490	gcaatagctcggacgcaalctgttgagagacaaggaaccccccaagccaagcccccaaggaga	549
Dd	481	GCAATAGCTCGAGACCAATCTGTGAGAGACAGGAGCCCCCACCACGACGAGCCCCAGAAA	540
Oy	550	ccccagggccccccggcgcaaggcccatcactgtccaaagcccaactgaagcctggccccagaact	609
Dd	541	CCCAGGGCCCCCGGCGCCAGGCCCATCTACTGTCCACCCCACTAAACCTTGCGCCAGAACTT	600
Oy	610	cacaaggacacctcacaacccgacccgctggaggtgccccggagggcgctgcggttgcgcgcatcc	669
Dd	601	CACAGGAACTCTCCACCGCGCCCGTGGAGAGTCCCGGGGGCCGTGCGGTGTGCGCCATTC	660
Oy	670	tgggcctggccttgatgcttgaggctgtgctgcgccttgacatcctgctgcgcctgtacc	729
Dd	661	TGGGCTCTGGGCTGTGTGTGGGTGTGTGGGCCCCCTGGCCATCTCTGCGGCTGTATAC	720
Oy	730	tgtctccgagaggagacagagggctgccccccgatagccacaagaagcccccttggaggaggaatt	789
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Oy	790	tccgagaccaccaaccacaagaagagcagcgcgcacatccacaccttggccaagatctgac	849
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Dd	841	CT 842	
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DEFINITION	Homo sapiens ox40 gene for CD134 antigen, exons 1-7.		
ACCESSION	AJ277151		
VERSION	AJ277151.1 GI:8926701		
KEYWORDS	CD134 antigen; Ox40 gene; rat Ox40 antigen homologue.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	1 (bases 1 to 5150)		
JOURNAL MEDLINE REFERENCE	Latzza,U., Durkop,H., Schmittger,S., Ringeling,J., Etelbach,F., Hummel,M., Fonatsch,C. and Stein,H. The human Ox40 homolog: cDNA structure, expression and chromosomal assignment of the ACTR35 antigen Eur. J. Immunol. 24 (3), 677-683 (1994) 94170844		
AUTHORS	2 (bases 1 to 5150) Parkow,R., Durkop,H., Latzza,U., Krause,H., Kunzendorf,U., Pohl,T. and Bulfow-Paus,S. The HTRV-1 tax protein transcriptionally modulates Ox40 antigen expression		
TITLE	J. Immunol. 165 (1), 263-270 (2000) 20318724		
JOURNAL MEDLINE REFERENCE	3 (bases 1 to 5150)		

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source	ODYCRCKRAGQPLDSYKPCVDCAPCPCPGHSPEDNDACKRPTCTLAKHTLDPASN	
source	SSDILCEDRDPPATQPEQTQGPAPRPITVQPTETAMPRTSQSPSTRPEVPEGRVAAI	
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Db 3870	TGGGCCACCAAGGTGAGACGTGGGCCGCCGCCAGGCTGGAGCCGAGGCTGCTGGGGC	3929						
QY 912	gagcagggcaggtgtgaagccgcgtccgcgcagagctctgagccaaactctgacagcttc	971						
Db 3930	GAGCAGGGCAGGTGAGAGGCCCTCCGCCACACCTCTGGGCCAACTCTGACCCGTTTC	3989						
QY 972	tagtgcagatgtgcgtccctgcgctctctgtcttaagatlgccatgacatacctctgcgcc	1031						
Db 3990	TAGTGCAGATGCTGCGCTCGCGCTCTGCTGTACTGATGCATGCATACCTCGGCCCC	4049						
QY 1032	gcgaggaaccaataaaaccttggcag	1058						
Db 4050	GCGGAGCACCAATPAAAAAACCCTTGGCAG	4076						
RESULT 6	AL162741	11119 bp	DNA	linear	HTG 08-FEB-2002			
LOCUS	AL162741							
DEFINITION	Homo sapiens chromosome 1 clone RP5-902P8, *** SEQUENCING IN							
ACCESSION	AL162741							
VERSION	AL162741.24	GI:18643745						
KEYWORDS	HTG; HTGS_PHASE1; HTGS_ACTIVEFIN; HTGS_DRAFT; HTGS_FULLTOP.							
SOURCE	human.							
ORGANISM	Homo sapiens							
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
TITLE	1 (sites)							
JOURNAL	Harrison,E.							
COMMENT	Direct Submission							
	Submitted (07-FEB-2002) Wellcome Trust Sanger Institute, Hinxton,							
	Cambridgeshire, CB10 1SA, UK. E-mail enquiries:							
	humquery@sanger.ac.uk							
	On Feb 10, 2002 this sequence version replaced gi:18642353.							
	----- Genome Center							
	Center: Wellcome Trust Sanger Institute							
	Center code: SC							
	Web site: http://www.sanger.ac.uk							
	Contact: humquery@sanger.ac.uk							
	----- Project Information							
	Center project name: dj902P8							

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----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 16% of reads
Dye-terminator Big Dye; 83% of reads
Consensus quality: 110490 bases at least Q40
Consensus quality: 110677 bases at least Q30
Consensus quality: 110755 bases at least Q30
Insert size: 110819; sum-of-contigs
Insert size: 160089; 6.7% error; agarose-fp
Quality coverage: 8.36x in Q20 bases; sum-of-contigs quality
coverage: 5.95x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 4 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 42985: contig of 42985 bp in length
* 42986 43085: gap of 100 bp
* 43086 54937: contig of 11852 bp in length
* 54938 55037: gap of 100 bp
* 55038 67254: contig of 12217 bp in length
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* Query Match 19.6%; Score 207; DB 2; Length 111119;
* Best Local Similarity 100.0%; Pred. No. 1.9e-93;
* Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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* DB 21664 TGGGCCACCAAGGTGAGCTGGCCCGCCAGCGCTGAGCGCCGAGGCTGTGCGGC 21605
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* QY 912 gaggcaggcaggtgacgagcgtgcccgcacgctctctggcgaactctgacgcttc 971
*   |||||||
* DB 21604 GACGACAGGCGGTGAGCGCGCTGCCCGCCAGCTCTCGGCGCAACTCTGACCGTTC 21545
*   |||||||
* QY 972 taagtcagatggctgctcccgctctctgactgaatgacatgacatctgcccc 1031
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* DB 21484 GCGGAGACCAATATAAACTTGCGAG 21458
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LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
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AL390719 210944 bp DNA linear HTG 30-JAN-2002
Homo sapiens chromosome 1 clone RP11-465B22, *** SEQUENCING IN
PROGRESS ***, 29 unordered pieces.
AL390719
AL390719.25 GI:18476612
HTG; HTGS_PHASE1; HTGS_DRAFT.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (sites)
McLay, K.
Direct Submission
Submitted (24-JAN-2002) Wellcome Trust Sanger Institute, Hinxton,
Cambridgeshire, CB10 1SA, UK. E-mail enquiries:
humquerry@sanger.ac.uk Clone requests: clonerequests@sanger.ac.uk
On Feb 1, 2002 this sequence version replaced gi:16304463.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquerry@sanger.ac.uk
----- Project Information
Center project name: BA465B22
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: plasmid; 108752; 100% of reads
Chemistry: Dye-terminator ET-amersham; 2% of reads
Dye-terminator Big Dye; 97% of reads
Consensus quality: 201072 bases at least Q40
Consensus quality: 204266 bases at least Q30
Consensus quality: 206043 bases at least Q20
Insert size: 208144; sum-of-contigs
Insert size: 227650; 6.6% error; agarose-fp
Quality coverage: 5.63x in Q20 bases; sum-of-contigs quality
coverage: 5.53x in Q20 bases; agarose-fp
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 29 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
*
* 1 8088: contig of 8088 bp in length
* 8089 8168: gap of 100 bp
* 8169 23213: contig of 15025 bp in length
* 23214 23313: gap of 100 bp
* 23314 27220: contig of 3907 bp in length
* 27221 27320: gap of 100 bp
* 27321 30326: contig of 3006 bp in length
* 30327 30426: gap of 100 bp
* 30427 43166: contig of 12740 bp in length
* 43167 43266: gap of 100 bp
* 43267 47516: contig of 4250 bp in length
* 47517 47616: gap of 100 bp
* 47617 51392: contig of 3776 bp in length
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* 51493 60771: contig of 9279 bp in length
* 60772 60871: gap of 100 bp
* 60872 63164: contig of 2293 bp in length
* 63165 63264: gap of 100 bp
* 63265 69307: contig of 6043 bp in length
* 69308 69407: gap of 100 bp
* 69408 76647: contig of 7240 bp in length
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* 76748 98297: contig of 21550 bp in length
* 98298 98397: gap of 100 bp
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* 100782 100881: gap of 100 bp
* 100882 108287: contig of 7406 bp in length
* 108288 108387: gap of 100 bp
* 108388 116410: contig of 8023 bp in length
* 116411 116510: gap of 100 bp
* 116511 119166: contig of 2656 bp in length
* 119167 119266: gap of 100 bp
* 119267 121683: contig of 2417 bp in length
* 121684 121783: gap of 100 bp
* 121784 125415: contig of 3632 bp in length
* 125416 125515: gap of 100 bp
* 125516 132751: contig of 7236 bp in length
* 132752 132851: gap of 100 bp
* 132852 137874: contig of 5023 bp in length
* 137875 137974: gap of 100 bp
* 137975 147639: contig of 9665 bp in length
* 147640 147739: gap of 100 bp
* 147740 150747: contig of 3008 bp in length
* 150748 150847: gap of 100 bp
* 150848 154411: contig of 3564 bp in length
* 154412 154511: gap of 100 bp
* 154512 180672: contig of 26161 bp in length
* 180673 180772: gap of 100 bp
* 180773 187118: contig of 6346 bp in length
* 187119 187218: gap of 100 bp
* 187219 197762: contig of 10544 bp in length
* 197763 197862: gap of 100 bp
* 197863 203431: contig of 5569 bp in length
* 203432 203531: gap of 100 bp
* 203532 206862: contig of 3331 bp in length
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Best Local Similarity 100.0%; Pred. No. 1.8e-93;
Matches 207; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 912 gaccaaggcaggtgtgcaagcgccctgcccgcgaacgtccctgggccaactctgcaacgttc 971
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QY 972 taagtgcgatagtgctgcctccggtctctcttactagatgcatgcatatcactctgcgcc 1031
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DEFINITION AX134865  
ACCESSION AX134865  
VERSION AX134865.1 GI:14271353  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Polypeptides with non-natural primary signalling motifs  
JOURNAL Patent: WO 0132709-A 58 10-MAY-2001;  
Celltech Chiroscience Limited (GB)  
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Db 6 CCGAGGACCAAGAGGCTGCCCGCCGATGCCACAAAGCCCCCTGGGGAGGAGCAgTTCCGg 65  
Oy 795 acccccatccaagagagcagc 817  
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Db 66 ACCCCATCCAAAGAGGAGCAGCg 88  
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LOCUS AX134962  
DEFINITION Sequence 73 from Patent WO0132867.  
ACCESSION AX134962  
VERSION AX134962.1 GI:14271404  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Polypeptides with expanded primary signalling motifs  
JOURNAL Patent: WO 0132867-A 73 10-MAY-2001;  
Celltech Chiroscience Limited (GB)  
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Best Local Similarity 100.0%; Pred. No. 1.7e-30;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Oy 795 acccccatccaagagagcagc 817  
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Db 66 ACCCCATCCAAAGAGGAGCAGCg 88  
RESULT 10  
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LOCUS AX135075  
DEFINITION Sequence 88 from Patent WO0132866.  
ACCESSION AX135075  
VERSION AX135075.1 GI:14271470  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Hybrid adaptor receptors  
JOURNAL Patent: WO 0132866-A 88 10-MAY-2001;  
Celltech Chiroscience Limited (GB)  
FEATURES  
source 1. 117  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Adaptor receptor construction oligonucleotide  
F1340A"  
BASE COUNT 25 a 45 c 36 g 11 t  
ORIGIN  
Query Match 7.8%; Score 83; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 1.7e-30;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 735 cggagggaccagaggtgcggcccgatgccacaaagcccccctggggagagcagttccgg 794  
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Db 6 CCGAGGACCAAGAGGCTGCCCGCCGATGCCACAAAGCCCCCTGGGGAGGAGCAgTTCCGg 65  
Oy 795 acccccatccaagagagcagc 817  
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Db 66 ACCCCATCCAAAGAGGAGCAGCg 88  
RESULT 11  
AX134866/C 117 bp DNA linear PAT 29-MAY-2001  
LOCUS AX134866  
DEFINITION Sequence 59 from Patent WO0132709.  
ACCESSION AX134866  
VERSION AX134866.1 GI:14271354  
KEYWORDS  
SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Polypeptides with non-natural primary signalling motifs  
JOURNAL Patent: WO 0132709-A 59 10-MAY-2001;  
Celltech Chiroscience Limited (GB)  
FEATURES  
source 1. 117  
Location/Qualifiers  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Oligonucleotide for chimeric receptor construction"  
BASE COUNT 11 a 35 c 45 g 26 t  
ORIGIN  
Query Match 7.4%; Score 78; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.8e-28;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Oy 768 aagccccctggggagagcagttccgagcccccatccaagagagcagcagccac 827

Db 83 AGCCCCCTGGGGGAGGCGAGTTCCGACCCCATCCAGAGAGAGCGCGACGCCAC 24  
OY 828 tccacctgagccaagatc 845  
Db 23 TCCACCCTGGCCAGATC 6

## RESULT 12

AX134963/c

LOCUS AX134963 117 bp DNA linear PAT 29-MAY-2001  
DEFINITION Sequence 74 from Patent W00132867.  
ACCESSION AX134963  
VERSION AX134963.1 GI:14271405  
KEYWORDS

SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Polypeptides with expanded primary signalling motifs  
JOURNAL Patent: WO 0132867-A 74 10-MAY-2001;  
Celltech Chiroscience Limited (GB)

## FEATURES

source

1. 117  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Chimeric receptor construction oligonucleotide  
Fl340B"

BASE COUNT 11 a 35 c 45 g 26 t  
ORIGIN

Query Match 7.4%; Score 78; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.8e-28;  
Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 768 aagcccccctggggagagcagttccgagaccatccaaagagagcagcgccac 827  
Db 83 AGCCCCCTGGGGGAGGCGAGTTCCGACCCCATCCAGAGAGAGCGCGACGCCAC 24

OY 828 tccacctgagccaagatc 845  
Db 23 TCCACCCTGGCCAGATC 6

## RESULT 13

AX135076/c

LOCUS AX135076 117 bp DNA linear PAT 29-MAY-2001  
DEFINITION Sequence 89 from Patent W00132866.  
ACCESSION AX135076  
VERSION AX135076.1 GI:14271471  
KEYWORDS

SOURCE synthetic construct.  
ORGANISM synthetic construct.  
REFERENCE 1 (bases 1 to 117)  
AUTHORS Finney,H.M. and Lawson,A.D.  
TITLE Hybrid adaptor receptors  
JOURNAL Patent: WO 0132866-A 89 10-MAY-2001;  
Celltech Chiroscience Limited (GB)

## FEATURES

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1. 117  
/organism="synthetic construct"  
/db\_xref="taxon:32630"  
/note="Adaptor receptor construction oligonucleotide  
Fl340B"

BASE COUNT 11 a 35 c 45 g 26 t  
ORIGIN

Query Match 7.4%; Score 78; DB 6; Length 117;  
Best Local Similarity 100.0%; Pred. No. 5.8e-28;

Matches 78; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 768 aagcccccctggggagagcagttccgagaccatccaaagagagcagcgccac 827  
Db 83 AGCCCCCTGGGGGAGGCGAGTTCCGACCCCATCCAGAGAGAGCGCGACGCCAC 24

OY 828 tccacctgagccaagatc 845  
Db 23 TCCACCCTGGCCAGATC 6

## RESULT 14

HSHOX40MR/c

LOCUS HSHOX40MR 1373 bp mRNA linear PRI 13-MAY-1994  
DEFINITION H.sapiens mRNA for OX40 homologue.  
ACCESSION X75962  
VERSION X75962.1 GI:472957  
KEYWORDS OX40 antigen.  
SOURCE human.  
ORGANISM human sapiens  
REFERENCE 1 (bases 1 to 1373)  
AUTHORS Latza,U., Durkop,H., Schnitger,S., Ringeling,J., Eitelbach,F.,  
Hummel,M., Fonatsch,C. and Stein,H.  
TITLE The human OX40 homologue: cDNA structure, expression and chromosomal  
assignment of the AC35 antigen  
JOURNAL Eur. J. Immunol. 24 (3), 677-683 (1994)  
MEDLINE 94170844  
REFERENCE 2 (bases 1 to 1373)  
AUTHORS Latza,U.  
TITLE Direct Submission  
JOURNAL Submitted (16-DEC-1993) U. Latza, FU Berlin, Klinikum Steglitz,  
Institute of Pathology, Hindenburgdamm 30, 12200 Berlin, FRG

## FEATURES

source

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SSDACERDPPATPOTEOGPAPPTVOTPEAKPRISQGSTPVEYGGRAVAAT  
LGGLVIGLGLPLALLLRLRDQRLPPDAHRRPGGGSFPTIOEDQADAHSTLAK  
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sig\_peptide 6.. 89  
mat\_peptide 90.. 836  
/product="OX40 homologue"

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repeat\_region 959.. 1079  
polya\_signal 1341.. 1346  
polya\_site 1358

BASE COUNT 257 a 452 c 423 g 241 t  
ORIGIN

Query Match 3.0%; Score 32; DB 9; Length 1373;  
Best Local Similarity 100.0%; Pred. No. 6.6e-05;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 852 tgggcccaccagtgagcctgagcccgcc 883  
Db 930 TGGGCCCAACAGGTGAGCGTGGCCCGCC 899

## RESULT 15

AR019518

LOCUS AR019518 618 bp DNA linear PAT 05-DEC-1998

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DEFINITION Sequence 6 from patent US 5783665.
ACCESSION AR019518
VERSION AR019518.1 GI:3974632
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 618)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5783665-A 6 21-JUL-1998;
FEATURES
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BASE COUNT      148 a      187 c      151 g      132 t
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Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACACACGCGCTGCAAGCCTGGACCAA 431

RESULT 16
LOCUS      114933      618 bp      DNA      linear      PAT 02-APR-1996
DEFINITION Sequence 6 from patent US 5457035.
ACCESSION      114933
VERSION      114933.1 GI:1249842
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 618)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5457035-A 6 10-OCT-1995;
FEATURES
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BASE COUNT      148 a      187 c      151 g      132 t
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Query Match      2.6%; Score 28; DB 6; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0077;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACACACGCGCTGCAAGCCTGGACCAA 431

RESULT 17
LOCUS      MMOX40      883 bp      mRNA      linear      ROD 20-DEC-1993
DEFINITION M. musculus OX40.
ACCESSION      221674
VERSION      221674.1 GI:312827
KEYWORDS
  OX40.
SOURCE
  house mouse.
ORGANISM
  Mus musculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 883)
AUTHORS
  Calderhead, D. M., Buhmann, J. E., van den Eertwegh, A. J., Claassen, E.,
  Noelle, R. J. and Felli, H. P.
TITLE
  Cloning of mouse OX40: a T cell activation marker that may mediate
  T-B cell interactions

```

```

JOURNAL      J. Immunol. 151 (10), 5261-5271 (1993)
MEDLINE      94044750
REFERENCE      2 (bases 1 to 883)
AUTHORS
  Calderhead, D. M.
TITLE
  Direct Submission
JOURNAL
  Submitted (11-FEB-1993) David M Calderhead, Molecular Immunology,
  Bristol-Myers Squibb, Pharmaceutical Research Institute, 3005 First
  Ave., Seattle, WA, 98121, USA
FEATURES
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Best Local Similarity 100.0%; Pred. No. 0.0073;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 424 acaccagcctgcaagcctggaccac 451
Db 404 ACACACGCGCTGCAAGCCTGGACCAA 431

RESULT 18
LOCUS      AR019521      1317 bp      DNA      linear      PAT 05-DEC-1998
DEFINITION Sequence 10 from patent US 5783665.
ACCESSION      AR019521
VERSION      AR019521.1 GI:3974635
KEYWORDS
SOURCE
ORGANISM
REFERENCE
  1 (bases 1 to 1317)
AUTHORS
  Baum, P. R., Fanslow, W. C. III, Gayle, R. B. and Goodwin, R. G.
TITLE
  Cytokine which is a ligand for OX40
JOURNAL
  Patent: US 5783665-A 10 21-JUL-1998;
FEATURES
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    1.1317
    /organism="unknown"
BASE COUNT      322 a      417 c      337 g      241 t
ORIGIN

Query Match      2.6%; Score 28; DB 6; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.007;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 424 acaaccagcctgcaagcctggaccac 451  
Db 404 ACAACGAGCCTGCAGCCCTGACCAA 431

RESULT 19  
LOCUS 114936 1317 bp DNA linear PAT 02-APR-1996  
DEFINITION Sequence 10 from patent US 5457035.  
ACCESSION 114936  
VERSION 114936.1 GI:1249844  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 1317)  
AUTHORS Baum,P.R., Fanslow,W.C. III, Gayle,R.B. and Goodwin,R.G.  
TITLE Cyclokin which is a ligand for OX40  
JOURNAL Patent: US 5457035-A 10 10-OCT-1995;  
FEATURES  
source 1..1317  
/organism="unknown"  
BASE COUNT 322 a 417 c 337 g 241 t  
ORIGIN

Query Match 2.6%; Score 28; DB 6; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 0.007;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 acaaccagcctgcaagcctggaccac 451  
Db 404 ACAACGAGCCTGCAGCCCTGACCAA 431

RESULT 20  
LOCUS MMDNAX40 2907 bp DNA linear ROD 23-AUG-1995  
DEFINITION M.musculus ox40 gene.  
ACCESSION X85214  
VERSION X85214.1 GI:732818  
KEYWORDS OX40 gene.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 2907)  
AUTHORS Birkeland,M.L., Copeland,N.G., Gilbert,D.J., Jenkins,N.A. and Barclay,A.N.  
TITLE Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein  
JOURNAL Eur. J. Immunol. 25 (4), 926-930 (1995)  
MEDLINE 95255413  
REFERENCE 2 (bases 1 to 2907)  
AUTHORS Birkeland,M.L.  
TITLE Direct Submission  
JOURNAL Submitted (10-MAR-1995) M.L. Birkeland, University of Pennsylvania, School of Medicine, 535 Clinical Research Building, 415 Curie Blvd., Philadelphia PA 19103, USA  
COMMENT Sequence overlapping with that under the acc#21674.  
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2592..2679  
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.0062;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 acaaccagcctgcaagcctggaccac 451  
Db 1731 ACAACGAGCCTGCAGCCCTGACCAA 1758

RESULT 21  
LOCUS AC100470 60953 bp DNA linear HTG 22-NOV-2001  
DEFINITION Mus musculus clone RP23-139J18, LOW-PASS SEQUENCE SAMPLING.  
ACCESSION AC100470  
VERSION AC100470.1 GI:17047836  
KEYWORDS HTG; HTGS\_PHASE0.  
SOURCE house mouse.  
ORGANISM Mus musculus  
REFERENCE 1 (bases 1 to 60953)  
AUTHORS Birren,B., Linton,L., Nusbaum,C. and Lander,E.

TITLE  
JOURNAL  
REFERENCE  
AUTHORS

Mus musculus, clone RP23-139J18  
Unpublished  
2 (bases 1 to 60953)  
Birren, B., Linton, L., Nusbaum, C., Lander, E., Ali, A., Allen, N.,  
Anderson, S., Barna, N., Bastien, V., Boguslavsky, L., Boukhgalter, B.,  
Brown, A., Camarato, J., Campolano, A., Chang, J., Chazaro, B.,  
Chapel, Y., Collangelo, M., Collins, S., Collymore, A., Cook, A.,  
Cooper, P., DeRellano, K., Dewar, K., Diaz, J., Dodge, S., Ferro, S.,  
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Raymond, C., Retto, R., Rieback, M., Riley, R., Rise, C., Rogov, P.,  
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Seaman, S., Severy, P., Spencer, B., Stange-Thomann, N., Stojanovic, N.,  
Strauss, N., Subramanian, A., Talamas, J., Testaye, S., Theodore, J.,  
Topham, K., Travers, M., Travis, N., Trigilio, J., Vassiliev, H.,  
Viel, R., Vo, A., Wilson, B., Wu, X., Wyman, D., Ye, W.J., Young, G.,  
Zainoun, J., Zembek, L., Zimmer, A. and Zody, M.

Direct Submission  
Submitted (22-NOV-2001) Whitehead Institute/MIT Center for Genome  
Research, 320 Charles Street, Cambridge, MA 02141, USA  
All repeats were identified using RepeatMasker:  
Smit, A.F.A. & Green, P. (1996-1997)  
<http://ftp.genome.washington.edu/RM/RepeatMasker.html>

----- Genome Center -----  
Center: Whitehead Institute/ MIT Center for Genome Research  
Center code: WIBR  
Web site: <http://www.seq.wi.mit.edu>  
Contact: [sequence\\_submissions@genome.wi.mit.edu](mailto:sequence_submissions@genome.wi.mit.edu)  
----- Project Information -----  
Center project name: I15392  
Center clone name: 139\_J\_18

\* NOTE: This record contains 75 individual  
\* sequencing reads that have not been assembled into  
\* contigs. Runs of N are used to separate the reads  
\* and the order in which they appear is completely  
\* arbitrary. Low-pass sequence sampling is useful for  
\* identifying clones that may be gene-rich and allows  
\* overlap relationships among clones to be deduced.  
\* However, it should not be assumed that this clone  
\* will be sequenced to completion. In the event that  
\* the record is updated, the accession number will  
\* be preserved.

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803 1518: contig of 716 bp in length  
1519 1618: gap of 100 bp  
1619 2337: contig of 719 bp in length  
2338 2437: gap of 100 bp  
2438 3141: contig of 704 bp in length  
3142 3241: gap of 100 bp  
3242 3940: contig of 699 bp in length  
3941 4040: gap of 100 bp  
4041 4751: contig of 711 bp in length  
4752 4851: gap of 100 bp  
4852 5561: contig of 710 bp in length  
5562 5661: gap of 100 bp  
5662 6373: contig of 712 bp in length  
6374 6473: gap of 100 bp  
6474 7193: contig of 720 bp in length  
7194 7293: gap of 100 bp  
7294 8009: contig of 716 bp in length  
8010 8109: gap of 100 bp  
8110 8802: contig of 693 bp in length  
8803 8902: gap of 100 bp

8903 9624: contig of 722 bp in length  
9625 9724: gap of 100 bp  
9725 10445: contig of 721 bp in length  
10446 10545: gap of 100 bp  
10546 11263: contig of 718 bp in length  
11264 11363: gap of 100 bp  
11364 12072: contig of 709 bp in length  
12073 12172: gap of 100 bp  
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12955 13673: contig of 719 bp in length  
13674 13773: gap of 100 bp  
13774 14492: contig of 719 bp in length  
14493 14592: gap of 100 bp  
14593 15303: contig of 711 bp in length  
15304 15403: gap of 100 bp  
15404 16120: contig of 717 bp in length  
16121 16220: gap of 100 bp  
16221 16917: contig of 697 bp in length  
16918 17017: gap of 100 bp  
17018 17727: contig of 710 bp in length  
17728 17827: gap of 100 bp  
17828 18550: contig of 723 bp in length  
18551 18650: gap of 100 bp  
18651 19370: contig of 720 bp in length  
19371 19470: gap of 100 bp  
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20167 20266: gap of 100 bp  
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22597 22696: gap of 100 bp  
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26666 26765: gap of 100 bp  
26766 27465: contig of 700 bp in length  
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31685 32382: contig of 698 bp in length  
32383 32482: gap of 100 bp  
32483 33190: contig of 708 bp in length  
33191 33290: gap of 100 bp  
33291 33966: contig of 706 bp in length  
33967 34096: gap of 100 bp  
34097 34814: contig of 718 bp in length  
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34915 35630: contig of 716 bp in length  
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35731 36463: contig of 733 bp in length  
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37292 37391: gap of 100 bp  
37392 38114: contig of 723 bp in length  
38115 38214: gap of 100 bp  
38215 38953: contig of 739 bp in length

```

* 38954 39053: gap of 100 bp
* 39054 39779: contig of 726 bp in length
* 39780 39879: gap of 100 bp
* 39880 40588: contig of 709 bp in length
* 40589 40688: gap of 100 bp
* 40689 41386: contig of 698 bp in length
* 41387 41486: gap of 100 bp
* 41487 42162: contig of 676 bp in length
* 42163 42262: gap of 100 bp
* 42263 42983: contig of 721 bp in length
* 42984 43083: gap of 100 bp
* 43084 43809: contig of 726 bp in length
* 43810 43909: gap of 100 bp
* 43910 44634: contig of 725 bp in length
* 44635 44734: gap of 100 bp
* 44735 45461: contig of 727 bp in length
* 45462 45561: gap of 100 bp
* 45562 46280: contig of 719 bp in length
* 46281 46380: gap of 100 bp
* 46381 47104: contig of 724 bp in length
* 47105 47204: gap of 100 bp
* 47205 47912: contig of 708 bp in length
* 47913 48012: gap of 100 bp
* 48013 48713: contig of 701 bp in length
* 48714 48813: gap of 100 bp
* 48814 49506: contig of 693 bp in length
* 49507 49606: gap of 100 bp
* 49607 50333: contig of 727 bp in length
* 50334 50433: gap of 100 bp
* 50434 51151: contig of 718 bp in length
* 51152 51251: gap of 100 bp
* 51252 51977: contig of 726 bp in length
* 51978 52077: gap of 100 bp
* 52078 52796: contig of 719 bp in length
* 52797 52896: gap of 100 bp
* 52897 53617: contig of 721 bp in length
* 53618 53717: gap of 100 bp
* 53718 54419: contig of 702 bp in length
* 54420 54519: gap of 100 bp
* 54520 55229: contig of 710 bp in length
* 55230 55329: gap of 100 bp
* 55330 56023: contig of 694 bp in length
* 56024 56123: gap of 100 bp

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Query Match 2.6%; Score 28; DB 2; Length 60953;  
 Best Local Similarity 100.0%; Pred. No. 0.0041;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaaccagcctgcaagcctggaccac 451  
 Db 30950 ACAACCAAGCCTGCACGCCCTGGACCAA 30923

RESULT 22  
 AL627204 253111 bp DNA linear HTG 27-OCT-2001  
 LOCUS  
 DEFINITION Mus musculus chromosome 4 clone RP23-118E21, \*\*\* SEQUENCING IN  
 PROGRESS \*\*\*, in unordered pieces.  
 ACCESSION AL627204.5 GI:16596721  
 VERSION HTG: HTGS\_PHASe1; HTGS\_DRAFT.  
 KEYWORDS  
 SOURCE  
 ORGANISM  
 Mus musculus.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 Submitted (26-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,  
 CB10 1SA, UK. E-mail enquiries: humquerry@sanger.ac.uk  
 Requests: clonerequests@sanger.ac.uk  
 On Nov 2, 2001 this sequence version replaced gi:16416310.  
 ----- Genome Center

Center: Sanger Centre  
 Center code: SC  
 Web site: <http://www.sanger.ac.uk>  
 Contact: humquerry@sanger.ac.uk  
 ----- Project Information  
 Center project name: bm118E21  
 ----- Summary Statistics  
 Sequencing program: XGAP4; version 4.5  
 Sequencing vector: plasmid: 108752; 100% of reads  
 Chemistry: Dye-terminator Big Dye; 100% of reads  
 Consensus quality: 250604 bases at least Q40  
 Consensus quality: 251169 bases at least Q30  
 Consensus quality: 251526 bases at least Q20  
 Insert size: 252011; sum-of-contigs  
 Insert size: 263925; 8.0% error; agarose-fp  
 Quality coverage: 11.85x in Q20 bases; sum-of-contigs quality  
 coverage: 11.37x in Q20 bases; agarose-fp  
 -----  
 \* NOTE: This is a 'working draft' sequence.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

#### FEATURES

source  
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 /organism="Mus musculus"  
 /db\_xref="taxon:10090"  
 /chromosome="4"  
 /clone="RP23-118E21"  
 /clone\_1lb="RPCT-23"  
 1..23621  
 /note="assembly\_fragment:05628  
 fragment\_chain:1  
 vector\_side:left"  
 23722..26584  
 /note="assembly\_fragment:07355  
 fragment\_chain:1"  
 26685..32762  
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 32863..56771  
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 61416..124554  
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 138558..179038  
 /note="assembly\_fragment:00567  
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 179139..210421  
 /note="assembly\_fragment:00017  
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 210522..2224019  
 /note="assembly\_fragment:07085  
 fragment\_chain:2"  
 224120..227775  
 /note="assembly\_fragment:01289  
 fragment\_chain:3"  
 227876..2253111  
 /note="assembly\_fragment:03553  
 fragment\_chain:3  
 clone\_end:77  
 vector\_side:right"  
 misc\_count 65488 a 61670 c 60569 g 64276 t 1108 others

BASE COUNT 65488 a 61670 c 60569 g 64276 t 1108 others  
 ORIGIN

Query Match 2.6%; Score 28; DB 2; Length 253111;  
 Best Local Similarity 100.0%; Pred. No. 0.0034;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 424 acaccagcctgcaagcctgaccac 451  
 ||||||||||||||||||||||||||||  
 Db 80147 ACACCAGGCTCTCAAGCCTGGACCA 80174

RESULT 23  
 AF389853 254197 bp DNA linear HTG 24-JAN-2002  
 LOCUS Mus musculus chromosome 4 clone RPCR-23-118E21 strain C57BL/6J,  
 DEFINITION WORKING DRAFT SEQUENCE, 13 ordered pieces.  
 ACCESSION AF389853  
 VERSION AF389853.1 GI:18307770  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
 SOURCE house mouse.  
 ORGANISM Mus musculus

REFERENCE  
 AUTHORS Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 254197)  
 Li, X., Bachmanov, A.A., Li, S., Chen, Z., Tordoff, M.G.,  
 Beauchamp, G.K., de Jong, P.J., Wu, C., Chen, L., West, D.B., Ross, D.A.,  
 Ohmen, J.D. and Reed, D.R.  
 Genetic, physical, and comparative map of the subtelomeric region  
 of mouse chromosome 4  
 Mamm. Genome 13 (1), 5-19 (2002)  
 21635547  
 11773963  
 2 (bases 1 to 254197)  
 Reed, D.R., Li, X., Bachmanov, A.A., Li, S., Chen, Z., Tordoff, M.G.,  
 Beauchamp, G.K., de Jong, P.J., Wu, C., Chen, L., West, D.B., Ross, D.A.  
 and Ohmen, J.D.  
 Direct Submission  
 Submitted (08-JUN-2001) Monell Chemical Senses Center, 3500 Market  
 St, Philadelphia, PA 19104, USA

TITLE  
 JOURNAL  
 MEDLINE  
 PUBMED  
 REFERENCE  
 AUTHORS

COMMENT

\* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 13 contigs. Gaps between the contigs  
 \* are represented as runs of N. The order of the pieces  
 \* is believed to be correct as given, however the sizes  
 \* of the gaps between them are based on estimates that have  
 \* provided by the submittor.  
 \* This sequence will be replaced  
 \* by the finished sequence as soon as it is available and  
 \* the accession number will be preserved.  
 \* 1 32448: contig of 32448 bp in length  
 \* 32449 32548: gap of unknown length  
 \* 32549 56900: contig of 24352 bp in length  
 \* 56901 57000: gap of unknown length  
 \* 57001 115350: contig of 58350 bp in length  
 \* 115351 115450: gap of unknown length  
 \* 115451 118046: contig of 2596 bp in length  
 \* 118047 118146: gap of unknown length  
 \* 118147 123765: contig of 5619 bp in length  
 \* 123766 123865: gap of unknown length  
 \* 123866 124811: contig of 946 bp in length  
 \* 124812 124911: gap of unknown length  
 \* 124912 132552: contig of 7341 bp in length  
 \* 132553 132552: gap of unknown length  
 \* 132553 154052: contig of 21700 bp in length  
 \* 154053 154152: gap of unknown length  
 \* 154153 183134: contig of 28982 bp in length  
 \* 183135 183234: gap of unknown length  
 \* 183235 197716: contig of 14482 bp in length  
 \* 197717 223095: contig of 25279 bp in length  
 \* 223096 223195: gap of unknown length  
 \* 223196 227717: contig of 4522 bp in length  
 \* 227718 254197: gap of unknown length  
 \* 254197 254197: contig of 26380 bp in length.  
 Location/Qualifiers  
 1. 254197

Query Match 2.6%; Score 28; DB 2; Length 254197;  
 Best Local Similarity 100.0%; Pred. No. 0.0034;  
 Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 424 acaccagcctgcaagcctgaccac 451  
 ||||||||||||||||||||||||||||  
 Db 201227 ACACCAGGCTCTCAAGCCTGGACCA 201254

RESULT 24  
 AX251339 5148 bp DNA linear PAT 05-OCT-2001  
 LOCUS Sequence 307 from Patent WO0168912.  
 DEFINITION AX251339  
 ACCESSION AX251339  
 VERSION AX251339.1 GI:15984762  
 KEYWORDS

SOURCE  
 ORGANISM  
 REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL

FEATURES  
 source  
 1. 5148  
 /organism="synthetic construct"  
 /db\_xref="taxon:32630"  
 /note="Chemically treated genomic DNA (Homo sapiens)"  
 BASE COUNT 871 a 182 c 1479 g 2615 t 1 others  
 ORIGIN

Query Match 2.2%; Score 23; DB 6; Length 5148;  
 Best Local Similarity 100.0%; Pred. No. 1.9;  
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Oy 5 agagacgagatgctgctgaggg 27  
 ||||||||||||||||||||||||  
 Db 4796 AGAGACGAGATGCTGCTGAGGG 4818

RESULT 25  
 AC007905 104480 bp DNA linear HTG 03-OCT-2000  
 LOCUS Homo sapiens chromosome 16q24.3 clone RP4-754F23, WORKING DRAFT  
 DEFINITION SEQUENCE, 35 ordered pieces.  
 ACCESSION AC007905  
 VERSION AC007905.2 GI:10280722  
 KEYWORDS HTG; HTGS\_PHASE2; HTGS\_DRAFT.  
 SOURCE human.  
 ORGANISM Homo sapiens

REFERENCE  
 AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 1 (bases 1 to 104480)  
 Kremmidiotis, G., Gardner, A.E., Callen, D.F. and Sutherland, G.R.  
 Large Scale Sequencing of the Chromosome 16 region q24.3  
 JOURNAL unpublished  
 TITLE 2 (bases 1 to 104480)  
 REFERENCE  
 AUTHORS Kremmidiotis, G., Gardner, A.E., Callen, D.F. and Sutherland, G.R.  
 Direct Submission  
 Submitted (24-JUN-1999) Cytogenetics & Molecular Genetics, Women's  
 & Children's Hospital, 72 King William Rd, Adelaide, SA 5006,



## COMMENT

Australia  
On Sep 23, 2000 this sequence version replaced gi:5174819.  
-----  
Genome Centre : CytoGenetics & Molecular Genetics  
Centre Code : CMGCMCH  
Website: <http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html>  
-----  
\* NOTE: This is a 'working draft' sequence. It currently  
\* consists of 35 contigs. Gaps between the contigs  
\* are represented as runs of N. The order of the pieces  
\* is believed to be correct as given, however the sizes  
\* of the gaps between them are based on estimates that have  
\* been provided by the submittor.  
\* This sequence will be replaced  
\* by the finished sequence as soon as it is available and  
\* the accession number will be preserved.  
1 1479: contig of 1479 bp in length  
1480 1487: gap of unknown length  
1488 6699: contig of 5212 bp in length  
6700 6707: gap of unknown length  
6708 10905: contig of 4198 bp in length  
10906 10912: gap of unknown length  
10913 11733: contig of 821 bp in length  
11734 11740: gap of unknown length  
11741 12602: contig of 862 bp in length  
12603 12609: gap of unknown length  
12610 13856: contig of 1247 bp in length  
13857 13863: gap of unknown length  
13864 20018: contig of 6155 bp in length  
20019 20025: gap of unknown length  
20026 21942: contig of 1917 bp in length  
21943 21949: gap of unknown length  
21950 23920: contig of 1971 bp in length  
23921 23927: gap of unknown length  
23928 24860: contig of 933 bp in length  
24861 24867: gap of unknown length  
24868 29279: contig of 4412 bp in length  
29280 29286: gap of unknown length  
29287 29772: contig of 486 bp in length  
29773 29779: gap of unknown length  
29780 32411: contig of 2632 bp in length  
32412 32418: gap of unknown length  
32419 33145: contig of 727 bp in length  
33146 33152: gap of unknown length  
33153 34862: contig of 1710 bp in length  
34863 34869: gap of unknown length  
34870 36643: contig of 1774 bp in length  
36644 36650: gap of unknown length  
36651 37348: contig of 698 bp in length  
37349 37355: gap of unknown length  
37356 42174: contig of 4819 bp in length  
42175 42182: gap of unknown length  
42183 45604: contig of 3423 bp in length  
45605 45611: gap of unknown length  
45612 48485: contig of 2874 bp in length  
48486 48492: gap of unknown length  
48493 49845: contig of 1353 bp in length  
49846 49852: gap of unknown length  
49853 51199: contig of 1347 bp in length  
51200 51206: gap of unknown length  
51207 51513: contig of 307 bp in length  
51514 51520: gap of unknown length  
51521 52180: contig of 660 bp in length  
52181 52187: gap of unknown length  
52188 60026: contig of 7839 bp in length  
60027 60033: gap of unknown length  
60034 64699: contig of 4666 bp in length  
64700 64706: gap of unknown length  
64707 69136: contig of 4430 bp in length  
69137 69143: gap of unknown length  
69144 73347: contig of 4204 bp in length  
73348 73354: gap of unknown length  
73355 82462: contig of 9108 bp in length

\* 82463 82469: gap of unknown length  
\* 82470 84166: contig of 1697 bp in length  
\* 84167 84173: gap of unknown length  
\* 84174 84822: contig of 649 bp in length  
\* 84823 84829: gap of unknown length  
\* 84830 99511: contig of 14682 bp in length  
\* 99512 99518: gap of unknown length  
\* 99519 101087: contig of 1569 bp in length  
\* 101088 101094: gap of unknown length  
\* 101095 103316: contig of 2222 bp in length  
\* 103317 103323: gap of unknown length  
\* 103324 104480: contig of 1157 bp in length.  
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FEATURES  
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/db\_xref="taxon:9606"  
/chromosome="16q24.3"  
/clone="RP4-754F23"  
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BASE COUNT 23140 a 28756 c 29631 g 22706 t 247 others  
ORIGIN  
Query Match 2.2%; Score 23; DB 2; Length 104480;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 671 ggagctgggagctgctgctggagc 693  
Db 6816 GGgCCTGGgCCTGGTGTGGGgC 6838  
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RESULT 26  
AB003911 877 bp mRNA linear MAM 05-FEB-1999  
LOCUS  
DEFINITION Rabbit mRNA for OX40 precursor, partial cds.  
ACCESSION AB003911  
VERSION AB003911.1 GI:2114107  
KEYWORDS OX40.  
SOURCE Oryctolagus cuniculus (sub\_species:domesticus, strain:Chdb:HM)  
ORGANISM Oryctolagus cuniculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
REFERENCE  
AUTHORS Isono, T.  
TITLE Direct Submission  
JOURNAL Submitted (14-MAY-1997) Takahiro Isono, Shiga University of Medical  
Science, Central Research Laboratory, Seta Tsukinowachou, Otsu,  
Shiga 520-2192, Japan (E-mail: [isono@belle.shiga-med.ac.jp](mailto:isono@belle.shiga-med.ac.jp),  
Tel:81-775-48-2308, Fax:81-775-48-2048)  
2 (sites)  
REFERENCE  
AUTHORS Isono, T. and Seto, A.  
TITLE Expression of OX40 and OX40 ligand genes in rabbit  
JOURNAL HTLV-I-transformed T cell lines  
FEATURES  
Unpublished (1997)  
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1..877  
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/strain="Chdb:HM"  
/sub\_species="domesticus"  
/db\_xref="taxon:9986"  
/cell\_line="H446"  
/cell\_type="HTLV-I-transformed T cell"  
1..54  
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/codon\_start=1  
/product="OX40 precursor"  
/protein\_id="BAA20059.1"  
/db\_xref="GI:2114108"  
/translation="GTAAGAGATLLGILGAEPRPCVGDPTYPGGRRCLEQPGY  
GVNSRCNSODPTICHPGEPGRYNEAVNYOACPCPCQCRNRSSSEQDCTHTPTVCR  
CRPGTPLNGTKHGVDCAPCPGHFSGGNNRACRWCTLAGKRTDAPASSIAYC  
EDRSSLATQPMETPSAPYRPPTARTSTAMPRTAQPSPPTLEASKPDLAIVLSIGIG

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55...801  
/product="OX40"  
BASE COUNT 157 a 324 c 275 g 121 t  
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 25;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 440 gccctggaccactgcacct 460  
Db 408 GCCCTGGACCACTGCACCTT 428

RESULT 27  
LOCUS BC002494 1420 bp mRNA linear PRI 12-JUL-2001  
DEFINITION Homo sapiens, clone IMAGE:3050476, mRNA, partial cds.  
ACCESSION BC002494  
VERSION BC002494.1 GI:12803350  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
TITLE 1 (bases 1 to 1420)  
JOURNAL Strausberg, R.  
Direct Submission  
Submitted (05-FEB-2001) National Institutes of Health, Mammalian  
Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA

REMARK  
COMMENT NIH-MGC Project URL: http://mgc.nci.nih.gov  
Contact: MGC help desk  
Email: cgabs-remail.nih.gov

Tissue Procurement: ATCC/DCRD/PTP  
CDNA Library Preparation: Rubin Laboratory  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: National Institutes of Health Intramural  
Sequencing Center (NISC),  
Gaithersburg, Maryland;  
Web site: http://www.nisc.nih.gov/  
Contact: nisc\_mgc@nsl.nih.gov  
Shevchenko, Y., Weisberg, K.D., Beckstrom-Sternberg, S.M.,  
Benjamin, B., Blakesley, R.W., Bouffard, G.G., Brinkley, C., Brooks, S.,  
Dietrich, N.L., Guan, X., Gupta, J., Ho, S.-L., Karlins, E., Legaspi, R.,  
Lim, M., Maduro, O.L., Mastello, C., Mastrian, S.D., McCloskey, J.C.,  
McDowell, J., Pearson, R., Snyder, B., Stantirlop, S., Thomas, P.J.,  
Tlonsong, E.E., Touchman, J.W., Tsurgon, C., Vogt, J.L., Walker, M.A.,  
Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found  
through the I.M.A.G.E. Consortium/LNL at: http://image.lnl.gov  
Series: IRAL Plate: 4 Row: e Column: 1  
This clone was selected for full length sequencing because it  
passed the following selection criteria: Genomescan gene  
prediction.

FEATURES  
source  
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/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
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/issue\_type="Skin, melanotic melanoma."  
/clone\_lib="NIH-MGC-20"  
/lab\_host="DH10B-R"  
/note="Vector: pOTB7"  
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/product="Unknown (protein for IMAGE:3050476)"  
/protein\_id="AAH02494.1"  
/db\_xref="GI:12803351"

CDS

/translation="ARGASRGVGSNAAMESTLIGAGIVIAEALQNLAMLEWVIMLT  
FLGDKILFLFFPAAYVASRRVGIWISLITELNLIFFWFLFGDRPFVWVHSG  
YSSAPAOVHOPSSCETGSPGSGCHMTGAAMPIMTALSSQVATRRASRVVYMP  
SLAVCFELAVGISRFILAHPHOVLAITGAVIGMTPTPVERELSTFGLTAL  
ALMGCSLWYTLFTIGLIDLSISLAFWCRCRPRVHVDSPFASLSDSCAALGIC  
IALHSPCAQVRAOLGNGCKTACLVLAGLIGLPLDMLGHPPOISLFTIFNFKITLW  
PCLVLALVMAVMEFSAQEPPIHSS"

Query Match 2.0%; Score 21; DB 9; Length 1420;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggtctgctggccccctgg 708  
Db 915 TGGGGCTGCTGGCCCCCTGG 935

RESULT 28  
LOCUS AX202231 1569 bp DNA linear PAT 30-AUG-2001  
DEFINITION Sequence 10 from Patent WO0153469.  
ACCESSION AX202231  
VERSION AX202231.1 GI:15392005  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
TITLE 1 (bases 1 to 1569)  
JOURNAL Bandman, O., Tang, Y.T., Azimzai, Y., Yue, H., Baughn, M.R.,  
Hillman, J.L., Lal, P., Wang, E., Gandhi, A.R., Policky, J.L. and  
Mathur, P.  
Phosphatases  
Patent: WO 0153469-A 10-26-JUL-2001;  
Incyte Genomics, Inc. (US)

FEATURES  
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1..1569  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/note="Incyte ID No: 1269556CB1"

BASE COUNT 263 a 505 c 444 g 357 t  
ORIGIN

Query Match 2.0%; Score 21; DB 6; Length 1569;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggtctgctggccccctgg 708  
Db 1089 TGGGGCTGCTGGCCCCCTGG 1109

RESULT 29  
LOCUS HSM802071 1632 bp mRNA linear PRI 18-FEB-2000  
DEFINITION Homo sapiens mRNA; CDNA DKFZp434L1226 (from clone DKFZp434L1226).  
ACCESSION AL137382  
VERSION AL137382.1 GI:6807912  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens

REFERENCE  
AUTHORS Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
TITLE 1 (bases 1 to 1632)  
JOURNAL Ansoorge, W., Wilkner, U., Mewes, H.W., Weil, B. and Wiemann, S.  
Direct Submission  
Submitted (15-JAN-2000) MIPS, Am Klopferplatz 18a, D-82152  
Martinsried, GERMANY  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer

Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de; sequenced by EMBL (European Molecular Biology Laboratories, Heidelberg/Germany) within the cDNA sequencing consortium of the German Genome Project.

This clone (DKFZP434L1226) is available at the RZPD in Berlin. Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further information about the clone and the sequencing project is available at <http://www.mips.biochem.mpg.de/proj/cDNA/>.

## FEATURES

SOURCE

Location/Qualifiers

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1. 1632
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKFZP434L1226"
/clone_id="434 (synonym: htes3). Vector pSport1; host
DH10B; sites NotI + SalI"
/dev_stage="adult"
/tissue_type="testis"
/map="16q24.3"
BASE COUNT      282 a      528 c      489 g      333 t
ORIGIN

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Query Match 2.0%; Score 21; DB 9; Length 1632;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 672 ggcctggcctgctgctgctg 692  
 ||||||||||||||||||||  
 Db 1006 GCCCTGGCCTGCTGCTGGG 1026

## RESULT 30

LOCUS BC021574 1634 bp mRNA linear PRI 18-JAN-2002  
 DEFINITION Homo sapiens, clone MGC:31975 IMAGE:4842511, mRNA, complete cds.  
 ACCESSION BC021574  
 VERSION BC021574.1 GI:18204314  
 KEYWORDS MGC.  
 SOURCE human.  
 ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 1634)  
 Strausberg, R.  
 Direct Submission  
 Submitted (14-JAN-2002) National Institutes of Health, Mammalian  
 Gene Collection (MGC), Cancer Genomics Office, National Cancer  
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
 USA

NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
 Contact: MGC help desk  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC

cDNA Library Preparation: Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Genome Sequence Centre,  
 BC Cancer Agency, Vancouver, BC, Canada  
 info@bgsc.bc.ca

Steven Jones, Jennifer Asano, Ian Bosdet, Yaron Butterfield,  
 Susanna Chan, Readman Chiu, Chris Fjell, Erin Garland, Ran Guin,  
 Letlicia Hsiao, Martin Krzywinski, Reta Kutsche, Oliver Lee, Soo  
 Sen Lee, Victor Ling, Carrie Mathewson, Candice McLeavy, Steven  
 Ness, Pawan Pandoh, Anna-Liisa Prabh, Parvaneh Saeedi, Jacqueline  
 Schein, Duane Smalhus, Michael Smith, Lorraine Spence, Jeff Stott,  
 Michael Thorne, Miranada Tsai, Natasha van den Bosch, Jill Vardy,  
 George Yang, Scott Zuyerdun, Marco Marra.

Clone distribution: MGC clone distribution information can be found  
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
 Series: IRAL Plate: 40 Row: 1 Column: 5  
 This clone was selected for full length sequencing because it  
 passed the following selection criteria: Hexamer frequency ORF

analysis, Genomescan gene prediction.

## FEATURES

SOURCE

Location/Qualifiers

```

1. 1634
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="MGC:31975 IMAGE:4842511"
/tissue_type="Eye, normal, pigmented retinal epithelium"
/clone_id="NIH-MGC-43"
/lab_host="DH10B-R"
/note="Vector: pORF7"
CDS
217..1257

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/codon_start=1
/product="Unknown (protein for MGC:31975)"
/protein_id="AAH21574.1"
/db_xref="GI:18204315"
/translation="MESLNGGIYAELONQAMLENNMIMTEFGDPKTLFLFYP
AAVTSRRVGTAVLMLISLITMLNLFKFLFGDPKRWVHESGYSQAPVQHPFS
SCETGPGSPSGCHMITGAAMPIMTALSSOATRASRWVMPSLACPELAVGLS
RIFLAFHPQVGLITGAVLGMIMTPRVMERELSFYGLTALAMGTSLLIYTLF
TLGLDLSWSISLAFKWCERPEMIVHSRPFASLSRDSGALGLIALHSPCYAQRRA
QLNGOKTACLVLAMGLLGPIDWLGHPQISLFYIFNFKYTLMPCLALVPAVHHA
FSAQEARPIHSS"
BASE COUNT      330 a      502 c      444 g      358 t
ORIGIN

```

Query Match 2.0%; Score 21; DB 9; Length 1634;  
 Best Local Similarity 100.0%; Pred. No. 23;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 688 tgggctgctgggccccctgg 708  
 ||||||||||||||||||||  
 Db 1088 TGGGCTGCTGGGCCCCCTGG 1108

Search completed: June 19, 2002, 02:21:10  
 Job time: 3946 sec

---

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:11:59 ; Search time 1591.56 Seconds

(Without alignments)  
8972.190 Million cell updates/sec

Title: US-09-852-845-1

Perfect score: 1058

Sequence: 1 cagcagagagcagatgtc.....cacataaaaccttgcag 1058

Scoring table: OLIGO\_NUC

Searched: 13736207 seqs, 674847542 residues

Word size: 0

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database:

EST:\*  
1: em\_estdb:\*  
2: em\_esthm:\*  
3: em\_estln:\*  
4: em\_estnu:\*  
5: em\_estov:\*  
6: em\_estpl:\*  
7: em\_estro:\*  
8: em\_hlc:\*  
9: gb\_estl:\*  
10: gb\_est2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_inv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	431	40.7	569	10 BG236062	BG236062 naf22a07.
2	391	37.0	544	10 BF063899	BF063899 7b90a10.x
3	386	36.5	512	10 BE349098	BE349098 ht50905.x
4	256	24.2	844	9 A1738634	A1738634 w11d02.x
5	240	22.7	393	9 AA306055	AA306055 EST177040
6	229	21.6	471	9 AA293499	AA293499 UI-H-BI2-
7	207	19.6	353	9 AM290885	AM290885 UI-H-BI2-
8	203	19.2	743	10 B1833441	B1833441 603088095
9	171	16.2	198	9 AM591834	AM591834 xx6b03.x
10	142	13.4	172	10 B1824093	B1824093 603039230
11	110	10.4	893	10 B1911081	B1911081 603069733
12	94	8.9	347	9 A1452801	A1452801 t350f10.x
13	92	8.7	92	10 B1821828	B1821828 603035715
14	82	7.8	398	9 AA970291	AA970291 op09h05.s
15	58	5.5	247	9 A1914208	A1914208 w476e10.x
16	45	4.3	668	9 A1991307	A1991307 w42d05.x
17	28	2.6	662	12 A2320958	A2320958 IM0041A08

18	24	2.3	630	9 AA501118	AA501118 vf97h05.r
19	21	2.0	342	9 AM889471	AM889471 RC6-NT002
20	21	2.0	477	9 A1823620	A1823620 w171d07.x
21	21	2.0	480	9 AA312871	AA312871 EST183529
22	21	2.0	482	9 A1126122	A1126122 qd77b04.x
23	21	2.0	545	9 AA477725	AA477725 z044f11.s
24	21	2.0	572	9 AL523655	AL523655 AL523655
25	21	2.0	585	10 BF810986	BF810986 CM2-C1017
26	21	2.0	636	9 A1264358	A1264358 q109f04.x
27	21	2.0	649	9 A1669655	A1669655 wcl2a05.x
28	21	2.0	650	10 BM006189	BM006189 603614011
29	21	2.0	653	10 BF725110	BF725110 bx12c11.y
30	21	2.0	683	10 BG422683	BG422683 602449189
31	21	2.0	692	10 BF036463	BF036463 601460214
32	21	2.0	736	9 AL578769	AL578769 AL578769
33	21	2.0	755	9 AL524354	AL524354 AL524354
34	21	2.0	759	10 B1258768	B1258768 602970353
35	21	2.0	762	10 BE312775	BE312775 601149543
36	21	2.0	774	10 BM048374	BM048374 603625618
37	21	2.0	779	10 BG478742	BG478742 602525664
38	21	2.0	789	9 AL572583	AL572583 AL572583
39	21	2.0	790	10 BG479022	BG479022 602525793
40	21	2.0	799	10 B1871312	B1871312 603392733
41	21	2.0	805	10 BM042047	BM042047 603616048
42	21	2.0	820	9 AL526414	AL526414 AL526414
43	21	2.0	827	10 AL578318	AL578318 AL578318
44	21	2.0	834	10 BF314033	BF314033 601901472
45	21	2.0	842	10 BG750265	BG750265 602709068
46	21	2.0	845	10 BG474551	BG474551 602517325
47	21	2.0	851	9 AL533389	AL533389 AL533389
48	21	2.0	854	9 AL524355	AL524355 AL524355
49	21	2.0	857	9 AL521417	AL521417 AL521417
50	21	2.0	864	9 AL521416	AL521416 AL521416

#### ALIGNMENTS

RESULT 1  
LOCUS BG236062/c  
DEFINITION naf22a07.x1 Soares\_NPBC Homo sapiens CDNA clone IMAGE:4141716 3'  
similar to SW:OX40\_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains  
MER22.cl TARI repetitive element ;, mRNA sequence.

ACCESSION BG236062  
VERSION BG236062  
KEYWORDS BG236062.1 GI:12749909  
SOURCE EST.

#### ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

#### REFERENCE

1 (bases 1 to 569)  
NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicgap.  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)

#### JOURNAL

COMMENT  
Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: M. Bento Soares, Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D. and M. Fatima  
Bonaldo, Ph.D.  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CCAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNLN at:  
Info@Image.lnl.gov  
Seq primer: -400p from Gbco  
High quality sequence stop: 478.  
Location/Qualifiers  
1. 569

#### FEATURES

SOURCE  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4141716"

```

/clone_11b="Soares_NBMC"
/tissue_type="lymphocyte"
/lab_host="DH10B (phage-resistant)"
/note="Organ: blood; Vector: pT73D-Pac; Site_1: NotI;
Site_2: EcoRI; 1st strand cDNA was primed with a Not I -
oligo(dt) primer [5',
TGTTACCAATCTGAAGTGGAGCGCCGCCGGATTTTTTTTTTTTTTTTTT
3']; double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Not I and cloned into the Not
I and Eco RI sites of the modified pT73 vector. Library
is normalized; constructed in the laboratory of M. Bento
Soares (University of Iowa)."
```

Query Match	40.7%	Score 431	DB 10	Length 569
Best Local Similarity	99.8%	Pred. No. 2.6e-192		
Matches 551	Conservative 0	Mismatches 0	Indels 1	Gaps 1

QY	507	atctgtgtggaagaaggaccccccaacacacgacgccccgaagaaacccaagccccggcc	566
Db	569	ATCTGTGAGAGACAGGAGGACCCCCAGCCACGACGACGCCCGAGAGACCAAGGACCCCGCCG	510
QY	567	aggccacatcaactgtctcaagcccaacttgaagcctctgtgcccagaacttcaacaggaaccttcaac	626
Db	509	AGGCCATTCACATGTCACACCCCACTGAACCTGTGGCCCAAGACTCACAAGGAGACCTTCAC	450
QY	627	cggccccggtggaaggtctcccggtggcggtgagttgtgcgcgcaactctgtggcctgtggcctgtgt	686
Db	449	CGGCCCTGTGAGAGTCCCGGGGGCCGTGCGGTGGCCATTCCTGAGCTGGGCTGGGCTGTGG	390
QY	687	ctgaggtctgtgtggcccccttgacactctctgtgtgccccctgtacactctccgaaggtaccag	746
Db	389	CTGGGGCTGTGCTGTGGGCCCCCTGGCCATTCCTGTGCGGCCCTGTACTGTCTCCGAGAGGACCG	330
QY	747	aggctgtccccccgaatgycacaaagaacccccctgtgggtggaagtcaggttttcggaacccccatcaa	806
Db	329	AGGCTGCCCCCGAGATGGCCACAGCCGCCCTGGGGAGGACAGTTTCGGAGACCCCATCCAA	270
QY	807	gaggtgacaggtgcgaagcccaactcaacccctgtgcgaagatctgaacctgtggccccacaagt	866
Db	269	GAGGAGCAGGGCGAGGCCACACTCCACTGGCCAGATCTGACC-TGGGCCACCAAGGT	211
QY	867	ggaacactgagcccccgcacaggtctgtagccccgaaggtctctgtgtgcgaaggtgcaaggtgtgc	926
Db	210	GGAGCGCTGGCCCCGCCCAAGCTGAGAGCCCGAGAGGCTTGTCTGGGGAGACAGGGCAGGTGC	151
QY	927	aggcgcgtctgcccgccagcagctctctgtggcacaacttgcacogtlttaagttgcagatgct	986
Db	150	AGGCGCGCTGGCCCCGCCCAAGCTCTGTGGGCGCAACTGTGACCGTTCTAGGTGCCGATGGCT	91
QY	987	gacctcgcgtctctgtcctaagtaatgtacatgtcaactctctctgcgcgcggagacacaataa	1046
Db	90	GCCTCGGCTCTCTCTTACTTACGTATGCATGCTACTCTCTGCCCCGGGAGCACCAATTA	31
QY	1047	aaacctgtgcag	1058
Db	30	AAACCTTGCGAG	19
RESULT	2		
LOCUS	BF063899/c		
DEFINITION	79b0d0a10.x1 NCI_CGAP_544 bp mRNA	544 bp	linear EST_16-OCT-2000
ACCESSION	BF063899		
VERSION	BF063899.1		
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

REFERENCE	Mammalia: Eutheria: Primates: Catarrhini, Homnidae; Homo. 1 (bases 1 to 544)
AUTHORS	NCI-CCAP <a href="http://www.ncbi.nlm.nih.gov/ncicgap">http://www.ncbi.nlm.nih.gov/ncicgap</a> .
TITLE	National Cancer Institute, Cancer Genome Anatomy Project (CCAP), Tumor Gene Index
JOURNAL	Unpublished (1997)
COMMENT	Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CUNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL, send email to:  
info@image.llnl.gov

Seq primer: -40UP from Glibco  
High quality sequence stop: 423.

## FEATURES

Location/Qualifiers  
1. .544

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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="IMAGE:3323226"  
/clone_1b="NCI_CGAP_c016"
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/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
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/note="Organ: colon; Vector: pT713D-Pac (Pharmacia) with a  
modified polylinker; Site_1: Not I; Site_2: Eco RI;
```

Plasmid DNA from the normalized library NCI-CGAP\_Col0 was prepared, and ss circles were made *in vitro*. Following HAB

purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA

from a pool of 5,000 clones made from the same library (cloneIDs 1057416-1061255, and 1144584-1145351).

Subtraction by Bento Soares and M. Fatima Bonaído. "

## ORIGIN

Query Match 37 0% Score 391 DB 10 Length 544

Best Local Similarity	99.88;	Pred. NO. 1.8e-173;	
Matches 511; Conservative	0;	Mismatches 0;	Indels 1; Gaps 14

[illegible][illegible]

```
007  AAAAAAAAAAAAAAAAAAAAAAAACAGCAGCCCAACAGGAGGCCAAGCCCCAAA CCC
DU   JIO  AAAAAAAAAAAAAAAAAAAAAAAACAGCAGCCCAACAGGAGGCCAAGCCCCAAA 45/
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[illegible]

CC7 450 CCACAGGATCCCCTCACCAGGATCCCCGGGCGGAGGTCGCGGC 39 /

[illegible]

D5 396 TCCCTGGGCGCCTAGTGTCTGGGSCGTCTAGGCCCCCCTGCCCCATTCCTGCTGCGCCCTGT 33/

QY 727 acctgctccgagagaccccgagagctgtcccccagatgccacaaagcccccctgtgggagagca /86  
|||||

Db 336 ACCTGCTCCGGAGGGACCAAGAGGCTGCCCCCGATGCCACACAGCCCCCTGGGGAGGCA 277

Qy 787 gtcttcgagaccccatccaaagagagagagccgacgcccactccacccctgtgccaatct 846

Db 276 GTTCCGGAACCCCATCCAGAAGAGAGAGAGCCGAGAGCCCACTCCACCCCTGGCCAAGATCT 217

QY 847 gaccttggtccacaaagtgcagctggcccgccagctggagcccgaggtctgc 906

Db 216 GACC-TGGGCCCAAGGTGGAGCGCTGGGCCCGCCGACGGCTGGAGCCCGGAGGGTCTGC 158

907 tgggcgagcagggcaggtgcaggccgcctgtcccgcgcacagctctctgtggccaattctgcac 966

Db 157 TGGGGGAGCAGGGGAGGCTGCAGGGCCCTGCCCCCGCCACGGCTCTCTGGGGCAACTCTGCAC 98

967 cgtctagatgcgatgagctgcctccgcgtctctctgattagtatgcatgatcaactcct 1026

```

Db 97 GGTTCAGTGCAGTGGCTGCTCCGCTCTGCTTACGTATGATGCATACCTCT 38
Oy 1027 gccgcggagaccacaataaaaccttggcag 1058
|||||
Db 37 GCCCGCGGACACATATAAACTTGCGCAG 6

RESULT 3
BE349098/c
LOCUS
DEFINITION BE349098 512 bp mRNA linear EST 18-JUL-2000
h5f0905.x1 NCI_CGAP_Mel15 Homo sapiens CDNA clone IMAGE:3150200 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.t1 PTR3 repetitive element ; , mRNA sequence.
BE349098
ACCESSION BE349098.1 GI:9261037
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 512)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Chris Moskaluk, M.D., Ph.D., Michael R.
Emmert-Buck, M.D., Ph.D. CDNA Library Preparation: Life
Technologies, Inc. CDNA Library Arrayed by: Christa Prange, The
I.M.A.G.E. Consortium DNA Sequencing by: Washington University
Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL, send email to:
info@image.llnl.gov
Seq primer: -40up from Gibco
High quality sequence stop: 427.
Location/Qualifiers
1. 512
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3150200"
/clone_lib="NCI_CGAP_Mel15"
/tissue_type="malignant melanoma, metastatic to lymph
node"
/lab_host="DH10B"
/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
Library constructed by Life Technologies."
BASE COUNT 73 a 162 c 200 g 77 t
ORIGIN
Query Match 36.5%; Score 386; DB 10; Length 512;
Best Local Similarity 99.8%; Pred. No. 4.2e-171;
Matches 506; Conservative 0; Mismatches 0; Indels 1; Gaps 1;
Oy 552 caggagcccccgagccacccatcacttcagcccaactgaagcttgcccaagaaactca 611
|||||
Db 512 CAGGGCCCCCGGACAGGCCATCTGTCAGGCCACTGAAGCTTGCCCCGAAACTCTA 453
612 caggagccctccacccgcccgtgagggtcccccgggggcccgtgaggttcgcgcacatctg 671
|||||
Db 452 CAGGGAACCTCCACCCGCGCGTGGAGGTCGCCGGGGCGCTGGCTTCCGCCATCCTG 393
672 ggcctggagctgtgtctgtgggtgtgtggccccctggcgcacatctgtgacctgtacctg 731
|||||
Db 392 GGCCTGGGCTGTGCTGTGGGCTGCTGGGCCCCCTGGCCATCTGCTGGCCTGTAACTTG 333
732 ctcgcgagagacacagagctgcgcgcgcagatgccacaagccccctgggggagagagcttcc 791
|||||
Db 332 CTCGCGAGGAGACCAAGCTGCCGCCGATGCCCAAGCCCCCTGGGGAGGAGCTTTC 273

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Oy 792 cggacccccatccaaagagagcagcagccagcccaactccacacttgcgaagatctgacct 851
|||||
Db 272 CGAGCCCCCATCCAGAGAGAGAGCGAGCGCCAGCCACTCCACCTCGGCCAAGATCTGACC - 212
852 tggcgcacaaagtgtgagcgtctggcccgcgcagagcttgagccggagggtctgtctgggc 911
|||||
Db 213 TGGGCCACCAAGGTGAGAGCGCTGGGGCCCCCGCAGGCTGTGAGCCCGAGGCTGTGCTGGGC 154
912 gaggagggcaggttgagcggcgccttcgcccgcacagctcttgggccaactctgcacagcttc 971
|||||
Db 153 GAGCAGGAGGAGGTGAGCGCGCTGCCCCGCCACGCTCTGGGCAACTCTGCACCGTTC 94
972 taagtgcagatgctgcgcctccgcgctctctgtcttaagatgcatgcatatacctcgcgcc 1031
|||||
Db 93 TAGGTGCGGATGCTGCTCCGCGCTCTGCTTACGTATGATGCATATACCTCTGCCCC 34
Oy 1032 gcggagaccacaataaaaccttggcag 1058
Db 33 GCGGAGCACACATATAAACTTGCGCAG 7

RESULT 4
A1738634/c
LOCUS
DEFINITION A1738634 844 bp mRNA linear EST 20-DEC-1999
w111d02.x1 NCI_CGAP_Col6 Homo sapiens CDNA clone IMAGE:2389923 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ; contains
MER22.t3 MSRI repetitive element ; , mRNA sequence.
A1738634
ACCESSION A1738634.1 GI:5100615
VERSION
KEYWORDS EST.
SOURCE human.
ORGANISM human.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 844)
AUTHORS NCI_CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
JOURNAL Tumor Gene Index
COMMENT Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
Tissue Procurement: Ilan Kirsch, M.D., Michael R. Emmert-Buck, M.D.,
Ph.D.
CDNA Library Preparation: M. Bento Soares, Ph.D.
CDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www.bio.llnl.gov/dbrrp/image/image.html
Insert length: 1075 Std Error: 0.00
Seq primer: -40up from Gibco
High quality sequence stop: 452.
Location/Qualifiers
1. 844
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2389923"
/clone_lib="NCI_CGAP_Col6"
/tissue_type="colon tumor, RER+"
/lab_host="DH10B"
/note="Organ: colon; Vector: pT73D-Pac (Pharmacia) with a
modified polylinker; Site_1: Not I; Site_2: Eco RI;
Plasmid DNA from the normalized library NCI_CGAP_Col6 was
prepared, and ss circles were made in vitro. Following HAP
purification, this DNA was used as tracer in a subtractive
hybridization reaction. The driver was PCR-amplified cDNAs
from a pool of 5,000 clones made from the same library
(cloneids 1057416-1061255, and 1144584-1145311).
Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 139 a 245 c 302 g 154 t 4 others
ORIGIN

```

Query Match 24.2%; Score 256; DB 9; Length 844;  
 Best Local Similarity 99.1%; Pred. No. 8.1e-110;  
 Matches 576; Conservative 0; Mismatches 4; Indels 1; Gaps 1;

478 tgcagccgagccagcaatagctcgaagcaatctgtgagagagagagagagagagagagc 537  
 |||||||  
 580 tgcagccgagccagcaatagctcgaagcaatctgtgagagagagagagagagagagc 521  
 |||||||  
 538 agccccaagc 597  
 |||||||  
 520 accccagc 461  
 |||||||  
 598 ggcccaagc 657  
 |||||||  
 460 ggcagc 401  
 |||||||  
 658 tgcagcaatcctgagagagagagagagagagagagagagagagagagc 717  
 |||||||  
 400 ttgcggccatcttgcggccatctgagagagagagagagagagagagc 341  
 |||||||  
 718 tgcagctgagc 777  
 |||||||  
 340 tgcagctgagc 281  
 |||||||  
 778 ggcagc 837  
 |||||||  
 280 ggcagc 221  
 |||||||  
 838 ccaagc 897  
 |||||||  
 220 ccaagc 162  
 |||||||  
 898 agc 957  
 |||||||  
 161 agc 102  
 |||||||  
 958 agc 1017  
 |||||||  
 101 actctgagc 42  
 |||||||  
 1018 atactctgagc 1058  
 |||||||  
 41 atactctgagc 1

RESULT 5  
 AA306055 393 bp mRNA linear EST 18-APR-1997  
 LOCUS EST177040 Jurkat T-cells VI Homo sapiens cDNA 5' end similar to  
 DEFINITION similar to OX40 homolog, mRNA sequence.  
 ACCESSION AA306055  
 VERSION AA306055.1 GI:1958383  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 393)  
 Adams, M.D., Kerlavage, A.R., Fleischmann, R.D., Fulmer, R.A., Bult  
 C.J., Lee, N.H., Kinkness, E.F., Weinstein, R.G., Gocayne, J.D., White  
 O., Sutton, G., Blake, J.A., Brandon, R.C., Man-Wai, C., Clayton, R.A.,  
 Cline, T.R., Cotton, M.D., Earle-Hughes, J., Fine, L.D., Fitzgerald,  
 L.M., Fitzhugh, W.M., Fritchman, J.L., Georgiades, N.S., Glodak, A.,  
 Kelley, J.C., Liu, L.-I., Marmaros, S.M., Merrick, J.M.,  
 Moreno-Palanges, R.F., McDonald, L.A., Nguyen, D.T., Pellegri, S.M.,  
 Phillips, C.A., Ryder, S.E., Scott, J.L., Saudek, D.M., Shiley, R.,  
 Small, K.V., Spriggs, T.A., Uterback, T.R., Weidman, J.F., Li, Y.,  
 Bednarek, D.P., Cao, L., Cepeda, M.A., Coleman, T.A., Collins, E.J.,  
 Dinko, D., Feng, D.-F., Ferlie, A., Fischer, C., Hastings, G.A., He, M.W.,  
 Hu, J.S., Greene, J.M., Gruber, J., Hudson, P., Kim, A.K., Kozak, D.L.,  
 Kunsch, C., Hungjun, J., Li, H., Weissner, P.S., Olsen, H., Raymond, L.,  
 Wei, Y.F., Wang, J., Xu, C., Yu, G.L., Ruben, S.M., Dillon, P.J., Fannon

JOURNAL  
 MEDLINE  
 COMMENT  
 Bioinformatics  
 The Institute for Genomic Research  
 9712 Medical Center Drive, Rockville, MD 20850 USA  
 Tel: 3018699056  
 Fax: 3018699423  
 Email: arkerlav@tigr.org  
 For clone availability, additional sequence and expression  
 information related to this EST, please check the TIGR Human Gene  
 Index (<http://www.tigr.org/tdb/hgi/hgi.html>)  
 Seq primer: M13 Reverse

FEATURES  
 source  
 Location/Qualifiers  
 1..393  
 /organism="Homo sapiens"  
 /db\_xref="ATCC (Inhost):160207"  
 /db\_xref="taxon:9606"  
 /clone\_id="Jurkat T-cells VI"  
 /cell\_type="T-lymphocyte"  
 /note="Vector: pBluescript SK-; Site\_1: EcoRI; Site\_2:  
 XhoI"

BASE COUNT 73 a 151 c 124 g 45 t  
 ORIGIN

Query Match 22.7%; Score 240; DB 9; Length 393;  
 Best Local Similarity 99.7%; Pred. No. 2.7e-102;  
 Matches 290; Conservative 0; Mismatches 1; Indels 0;

281 cagaagtggagc 340  
 |||||||  
 103 cagaagtggagc 162  
 |||||||  
 341 ccgagcggagc 400  
 |||||||  
 163 ccgagcggagc 222  
 |||||||  
 401 tccagagcactcttcccaagagagagagagagagagagagagagagagc 460  
 |||||||  
 223 tccagagcactcttcccaagagagagagagagagagagagagagagagc 282  
 |||||||  
 461 ggcctggagc 520  
 |||||||  
 283 ggcctggagc 342  
 |||||||  
 521 ggcagcggagagagagagagagagagagagagagagagagagagagc 571  
 |||||||  
 343 ggcagcggagagagagagagagagagagagagagagagagagagagc 393  
 |||||||

RESULT 6  
 AM293499/C 471 bp mRNA linear EST 16-JAN-2000  
 LOCUS AM293499/C  
 DEFINITION UI-H-B12-bhg-a-02-0-UI.s1 NCI-CGAP\_Sub4 Homo sapiens cDNA clone  
 IMAGE:2727458 3', mRNA sequence.  
 ACCESSION AM293499  
 VERSION AM293499.1 GI:6700135  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 471)  
 NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
 National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
 Tumor Gene Index  
 Unpublished (1997)  
 Contact: Robert Strausberg, Ph.D.





pool 1 : L1AM 3164-3167, 3716-3720, 3733-3735 (IMAGE Clonoids 1257096-1258631, 1469064-1470983, 1475592-1476743)  
 ) NCI CGAP\_Pcr2 pool 1 : L1AM 2457-2459, 2758-2759, 3063-3068 (IMAGE Clonoids 985608-986759, 1101192-1101959, 1217928-1220615) NCI CGAP\_Co10 pool 1 : L1AM 2644-2653, 2871-2872 (IMAGE Clonoids 1057416-1061255, 1144584-1145355)  
 ) Subtraction was performed as previously described [Bonaldo, Lennon & Soares (1996) : Normalization and Subtraction: Two Approaches To Facilitate Gene Discovery. Genome Research 6, 791-806.]  
 TAG\_L1B-NCI CGAP\_Lel12  
 TAG\_TISSUE-le1omyosarcoma  
 TAG\_SEQ-ATACG\*  
 48 a 127 g 75 t  
 103 c

Query Match	Similarity	Score	DB	Length
Best Local	Similarity	100.0%	Pred. No. 9.4e-87	
Matches	207	Conservative	0	Mismatches 0; Indels 0; Gaps 0;
QY	852	tgggccacacaaagctgagacgtgggcccgcgaagctgagaccgagagctctgtctgggc	911	
Db	242	tgggccccaacaaagctggaacgtggggcccccgcagagctgagaccgagagctgtgctgggc	183	
QY	912	gagcagggcaagctgcagggcgccctggcccgcacagctctctggccaactctgcacggttc	971	
Db	182	gagcagggcagctgcagggccgctgcctcccccgcacacctctctggcccaacatctccacacgttc	123	
QY	972	taaggctgcgaatgagctgcgtccgcgtctctgtactagatgatgcaatgcatcacctctgcgtccc	1031	
Db	122	taaggctgcgaatgagctgcgtccgcgtctctgtactagatgatgcaatgcatcacctctgcgtccc	63	

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Qy 1032 gcggygaccacaataaaaaaccttgccag 1058
      |||||
Db 62 GCGGACCAACAATAAAAACTTGGCAG 36

```

RESULT	8			
B1833441				
LOCUS		743 bp	mRNA	linear
DEFINITION	B1833441	603088095P1	NIH_MGC_120	homo sapiens cDNA clone IMAGE:5227195 5',
		mRNA sequence.		
ACCESSION	B1833441			
VERSION	B1833441.1	GI:15944991		
KEYWORDS	EST.			
SOURCE	human.			

ORGANISM	Homo sapiens
EUKARYOTE	Chordata; Craniata; Vertebrata; Euteleostomi
MAMMALIA	Eutheria; Primates; Catarrhini; Hominoidea; Homo
REFERENCE	1 (bases 1 to 743)
AUTHORS	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D.

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Plate: LLAM1571 row: m column: 24
High quality sequence stop: 659.
Location/Qualifiers
1..743
FEATURES
source
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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="522719"
/clone_lib="NH_MGC_120"
/lab_host="DH10B"
note="Organ: pooled pancreas and spleen; Vector

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BASE COUNT 135 a 275 c 235 g 98 t  
ORIGIN

Query Match 203:	19.2%	Score 203:	DB 10:	Length 743:
Best Local Similarity	100.0%	Pred. No.	7,7e-85:	
Matches	203:	Conservative	0:	Mismatches 0: Indels 0: Gaps 0:
QY	555	ggccccccggcagagccatcactgctccagccactgaagcctgycgcagaacctcaag	614	
DB	201	GGCCCCCGCGCGACGAGCCCATCTCCAGCCACCTGAAGCCTGGGCCGAGACCTTCAG	260	
QY	615	ggacctccaccgagccgctgaggctcccgaggggccgctgctgttcgcacatccctggagc	674	
DB	261	GGACCCCTCACCCCGCCGCGCTGGAGGGTCCCGGGGGCGCTGGCGTTGGCCCATCTCGGGCC	320	
QY	675	cctggagcctgctgctggagcctgctggagcccccggacatcctgctggccctgtactgcttc	734	
DB	321	CTGGGCGTGTGCTGTGGGGCTGCTGGAGCCCTTGCCATCTCTGTGGCCCTGTACGCTGC	380	
QY	735	cggaaaggacaaagctgtgcccc	757	
DB	381	CGAGGGACCAAGAGCTGCCCC	403	

RESULT	9
AW591834/c	
LOCUS	x86B03.x1 NC1-CCAP-Lym12 Homo sapiens cDNA clone IMAGE:2850509 3'
DEFINITION	mRNA sequence.
ACCESSION	AM591834
VERSION	AM591834.1 GI:7279000
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

Email: [cgapds-remail@lin.gov](mailto:cgapds-remail@lin.gov)  
Life Technologies catalog #: 11347-015  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution by: NCI-CGAP clone distribution Information can be  
found through the I.M.A.G.E. Consortium/ULMW at:  
[image.lnlnl.gov/image/html/1/resources.shtml](http://image.lnlnl.gov/image/html/1/resources.shtml)  
Seq primer: -400P from Gibco  
High quality sequence, stop: 197.

FEATURES	SOURCE
Location/Qualifiers	
1..198	
/organism="Homo sapiens"	
/db_xref="taxon:9606"	
/clone IMAGE:2850509"	
/clone_11b="NCI-CCAP_Lym12"	
/tissue_type="Lymphoma, follicular mixed small and large cell"	
/lab_host="DH10B"	
/note="Organ: lymph node; Vector: PCMV-SPORT6; Site: 1; Salt: Site 2; Note: Cloned unidirectionally. Primer:	

BASE COUNT	a	c	g	t	others
34	63	69	31	1	

	ORIGIN	
	Query Match	16.2%; Score 171; DB %; Length 198;
	Best Local Similarity	100.0%; Pred. No. 8.4e-70;
Matches	171; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
OY	888 tggagccggaagtctcgtctgaggacgacgagcgatgcagccgctgccgcaccacgc	947
Dd	177 TGGAGCCCGGAGGGCTTCTGTGGCAGACGAGGCAAGTGTCAGCGCCGCCCGGCACAGC	118
OY	948 tcctggggccaactctgcacaccttcaggtagtgcagatgagttgctcgtcctcttgaa	1007
Dd	117 TCCTGGGCCAACTCTGCACCCTTTAAAGTAGGATGCAGATGGCTCCGAGCTCTCTGTACG	58
OY	1008 tatcgatacatcaacctcctctgcacccgacgagcacacaataaaccttgtcag	1058
Dd	57 TATGGCATGCAVACCTCCTGTGCCCGGGGACACATAAAAACCTTGGCAC	7
RESULT	10	
B1824093		
LOCUS	60303230F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5180287 5'	linear EST 04-OCT-2001
DEFINITION	mRNA sequence.	
ACCESSION	B1824093	
VERSION	B1824093.1 GI:15935643	
KEYWORDS	EST.	
SOURCE	human.	
ORGANISM	Homo sapiens	
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
	Mammalia; Eutheraia; Primates; Catarrhini; Hominiidae; Homo.	
REFERENCE	NIH-MGC http://mgc.nci.nih.gov/.	
AUTHORS	NIH-MGC	(bases 1 to 172)
TITLE	National Institutes of Health, Mammalian Gene Collection (MGC)	
JOURNAL	Unpublished (1999)	
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LHAM149 row: k column: 08 High quality sequence start: 2 Location/Qualifiers	
FEATURES		
SOURCE	1..172	
	/organism="Homo sapiens"	
	/db_xref="taxon:3606"	
	/clone="IMAGE:5180287"	
	/clone_id="NIH_MGC_115"	
	/lab_host="DH10B"	
	/note="Organ: pooled brain, lung, testis; Vector: pCMW-SPORT6; Site:1: NotI; Site:2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; 1 male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC library."	
BASE COUNT	24 a	54 c 68 g 26 t
ORIGIN		
Query Match	13.4%; Score 142; DB 10; Length 172;	
Best Local Similarity	100.0%; Pred. NO. 3.e-56;	
Matches	142; Conservative	0; Mismatches 0; Indels 0; Gaps 0;

OY	39	gagcggcgccgtgtgcggctctctctctcttgaggcttggagcttgacacgctgaacggg	98
DB	31	GGCCCGGCGCGGTGTGCCTCTCTCTCCCTGGGCCCTGAGCACCCTGACGGGG	90
OY	99	ctccactctgttcggggagaccttaaccacgaacacgctgtctgccagagtgcaggca	158
DB	91	CTCCACTGTGTGGGGACACCTACCCCCAGCAACGACCGTGTGTCACAGATGCAAGCCA	150
OY	159	ggcaacgggatgttagccgct	180
DB	151	GGCACGGGATGTGTGACCGCT	172
RESULT 11			
LOCUS	B1911081	893 bp	mRNA linear EST 16-OCT-2001
DEFINITION	603069733P1 NIH_MGC_118 Homo sapiens cDNA clone IMAGE:5218473 5'		
ACCESSION	B1911081		
VERSION	B1911081.1	GI:16174620	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.		
TITLE	NIH-MGC http://mgc.nci.nih.gov/.		
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)		
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgapbs@mail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNLN at: http://image.lnl.gov Plate: LLM11549 row: b column: 10 High quality sequence start: 23 High quality sequence stop: 593. Location/Qualifiers 1..893 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image="5218473" /clone_lib="NIH_MGC_118" /tissue_type="Leukocyte" /lab_host="DH10B" /note="Vector: pCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA source: leukocytes from anonymous pool of non-activated adult donors. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.7 kb. Insert size range 1.2-3.3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH_MGC library."		
FEATURES	source		
BASE COUNT	171 a	300 c	272 g 150 t
ORIGIN			
Query Match	10.4%	Score 110;	DB 10; Length 893;
Best Local Similarity	100.0%;	Pred. No. 5.3e-41;	
Matches 110; Conservative	0;	Mismatches 0;	Indels 0; Gaps 0;
OY	254	gtcgaagccctcacatgttgttaacctagaagatggagtgaggaacagctgtgcac	313
DB	231	GTCGAAGCCCTCACACTGTGTAACTCTGAAGTAGTGAGTACGGAAACACTGTGCAC	290
OY	314	ggccacacagacacagctcgcgcgtccggcggcggcaccacgcccctgg	363
DB	291	GGCCACACAGACACAGTGTGCCGCTGCGGGCGGGCACCCAGCCCTGG	340

```
RESULT 12
LOCUS A1452801/C
DEFINITION t350f10.x1 Soares NSF_F8_9W_OT_PA_P_S1 Homo sapiens cDNA clone
IMAGE:2144971.3' similar to contains MER22.t3 MER22 repetitive
element ;, mRNA sequence.
ACCESSION A1452801
VERSION A1452801.1 GI:4287894
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 347)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert length: 1030 Std Error: 0.00
Seq primer: -400P from Gibco
High quality sequence stop: 323.
FEATURES
source
1..347
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2144971"
/clone_11b="Soares_NSF_F8_9W_OT_PA_P_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with
a modified polylinker; Site.1: Not I; Site.2: Eco RI;
Equal amounts of plasmid DNA from five normalized
libraries were mixed, and as circles were made in vitro.
Following HAP purification, this DNA was used as tracer in
a subtractive hybridization reaction. The driver was
PCR-amplified cDNAs from pools of 5,000 clones made from
the same 5 libraries. The pools consisted of the following
libraries and clones: Soares NBHSF pool 1:
309384-310919, 323208-325895 Soares NB2HP pool 1:
145032-147335, 147720-148103, 148872-149255, 15002 -
150407, 151176-152327 Soares NB2HR8-9W pool 1:
758280-760583, 772104-774407 Soares NBHPA pool 1:
304776-306311, 320136-322823, 326280-326663 Soares NBHOT
pool 1: 723720-726407, 739080-740999 Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 51 a 100 c 117 g 78 t 1 others
ORIGIN
Query Match 8.9%; Score 94; DB 9; Length 347;
Best Local Similarity 100.0%; Pred. No. 1.7e-33;
Matches 94; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 751 tgcctccgagatccacaagccccctggggagagcagttccggacccccatccaagagg 810
|||||
DB 331 TGCCCCCGGATGCCACAAGCCCCCTGGGGAGGAGTTCGCGAGACCCCATCAAGAGG 272
|||||
QY 811 agcaaggcagagccacatccacccctggccaagat 844
|||||
DB 271 AGCAGGCGAGCGCCACTCCACCTGCGCCAAAGAT 238
|||||
```

```
RESULT 13
LOCUS B1821828
DEFINITION 603035715F1 NIH_MGC_115 Homo sapiens cDNA clone IMAGE:5176899 5',
RNA sequence.
ACCESSION B1821828
```

```
VERSION B1821828.1 GI:15933378
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 92)
AUTHORS NIH-MGC http://mgc.ncbi.nlm.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Life technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LLM11440 row: n column: 04
High quality sequence stop: 92.
FEATURES
source
1..92
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5176899"
/clone_11b="NIH_MGC_115"
/lab_host="DH10B"
/note="Organ: pooled brain, lung, testis; Vector:
PCMV-SPORT6; Site.1: NotI; Site.2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
BASE COUNT 17 a 30 c 33 g 12 t
ORIGIN
Query Match 8.7%; Score 92; DB 10; Length 92;
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 92; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 89 cgtgacggggtccctactgtctggggagacactaccacgaacgagtcgtgcacga 148
|||||
DB 1 CGTGACGGGGCTCCACTGTGTCGGGAGACACCTAACCCACACGACCGGTGCGACGA 60
|||||
QY 149 gtgcagggcaggaacggagatgtgagccgct 180
|||||
DB 61 GTGCAGGCCAGGCAACGGGATGTGACCGCT 92
|||||
```

```
RESULT 14
LOCUS AA970291/C
DEFINITION op09h05.s1 NCI_CGAP_K16 Homo sapiens cDNA clone IMAGE:1575225 3'
similar to SW:OX40_HUMAN P43489 OX40L RECEPTOR PRECURSOR ;, mRNA
sequence.
ACCESSION AA970291
VERSION AA970291.1 GI:3145804
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 398)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
```

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: Stratagene, Inc.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbp/image/image.html  
Seq primer: -40m13 fwd. RT from Amersham  
High quality sequence stop: 180.

FEATURES  
source  
Location/Qualifiers  
1. .398  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1575225"  
/clone\_lib="NCI-CGAP\_K1d6"  
/sex="mixed"  
/tissue\_type="kidney tumor"  
/lab\_host="SOLR (kanamycin resistant)"  
/note="Organ: kidney; Vector: Bluescript SK-; Site: 1;  
EcoRI, Site 2; XhoI; Cloned unidirectionally. Primer:  
Oligo dT. Pooled kidney tumors. 5' adaptor sequence: 5'  
GAATCGGCACAG 3' adaptor sequence: 5'  
CTCAGAGTTTTTTTTTTTTT 3' Average insert size: 1.0 Kb."

BASE COUNT 61 a 125 c 146 g 66 t

ORIGIN

Query Match 7.8%; Score 82; DB 9; Length 386;  
Best Local Similarity 100.0%; Pred. No. 7.8e-28;  
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 857 ccaccaggtgagcgtgagcccccagcagctgagagcccgagagctgcctggcgagca 916  
|||||  
DB 189 CCACCAAGGTGACGCTGGGCCCGCCGAGCTGAGCCGAGGCTGCTGGCGCAGCA 130  
|||||

QY 917 gggcaggtgcagagcgagcctgcc 938  
|||||

DB 129 GGGCAGGTGACGCGCCCTGCC 108

RESULT 15  
AI914208 247 bp mRNA linear EST 17-DEC-1999  
LOCUS w076e10.x1 NCI-CGAP\_Lu24 Homo sapiens CDNA clone IMAGE:2337546 3',  
DEFINITION mRNA sequence.  
ACCESSION AI914208  
VERSION AI914208.1 GI:5634063  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 247)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
www-bio.llnl.gov/dbp/image/image.html  
Insert length: 373 Std Error: 0.00  
Seq primer: -40UP from Gibco.  
Location/Qualifiers

FEATURES

source  
1. .247  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2337546"  
/clone\_lib="NCI-CGAP\_Lu24"  
/tissue\_type="carcinoid"  
/lab\_host="DH10B"  
/note="Organ: Lung; Vector: pRT73D-Pac (Pharmacia) with a  
modified polylinker. Plasmid DNA from the normalized  
library NCI-CGAP\_Lu5 was prepared, and ss circles were  
made in vitro. Following Hsp purification, this DNA was  
used as tracer in a subtractive hybridization reaction.  
The driver was PCR-amplified cDNAs from a pool of 5,000  
clones made from the same library (cloneds  
1414920-1417991 and 1520904-1522439). Subtraction by Bento  
Soares and M. Fatima Bernaldo."

BASE COUNT 41 a 70 c 79 g 57 t

ORIGIN

Query Match 5.5%; Score 58; DB 9; Length 247;  
Best Local Similarity 99.1%; Pred. No. 1.5e-16;  
Matches 108; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 852 tgggcccacaaagtgcagcgtgagcccccagcagctgagagccgagagctgctgggc 911  
|||||  
DB 227 TGGGCCACCAAGGTGACGCTGGGCCCGCCGAGCTGAGCCCGAGGCTTGTCTGGGC 168  
|||||

QY 912 gaggcaggtgcagagcgagcgtgagcccgagcagctgcctggccaact 960  
|||||

DB 167 GAGCAGGCGCAGGTGACGCGCCCTGCCCGCCAGCGCTCTGGGCCACT 119  
|||||

RESULT 16  
AI991307 668 bp mRNA linear EST 09-MAR-2000  
LOCUS w142d05.x1 Soares\_Dieckgraefe.colon.NHCD Homo sapiens CDNA clone  
DEFINITION IMAGE:2522697 3' similar to SW:OX40\_HUMAN P43489 OX40L RECEPTOR  
PRECUSOR ;, mRNA sequence.  
ACCESSION AI991307  
VERSION AI991307.1 GI:5838212  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 668)  
NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgaps-remail.nih.gov  
This clone is available royalty-free through LLNL; contact the  
IMAGE Consortium (info@image.llnl.gov) for further information.  
Insert length: 797 Std Error: 0.00  
Seq primer: -40UP from Gibco  
High quality sequence stop: 217.

FEATURES  
source  
1. .668  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2522697"  
/clone\_lib="Soares\_Dieckgraefe.colon.NHCD"  
/tissue\_type="colonic mucosa from 3 patients with Crohn's  
disease"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: colon; Vector: pRT73D-Pac (Pharmacia) with a  
modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTTACCAATCTGAAGTGGAGGCGGCCCGCTTTTCTTTTCTTTT 3'],  
double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I



the Not I and Eco RI sites of the modified pT7T3 vector.  
RNA provided by Dr. Minoru Ko, Wayne State Univ. Library  
constructed and normalized by Bento Soares and M. Fatima  
Bonaldo.

BASE COUNT 144 a 196 c 152 g 138 t

ORIGIN

Query Match 2.3%; Score 24; DB 9; Length 630;  
Best Local Similarity 100.0%; Pred. No. 1.8;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 428 ccaggcctgcgaagccctggaccac 451  
|||||  
Db 233 CCAGGCTGCAAGCCCTGACCAC 256

RESULT 19  
AM889471/c 342 bp mRNA linear EST 24-MAY-2000  
LOCUS RC6-NT0029-280400-012-B08 NT0029 Homo sapiens CDNA, mRNA sequence.  
DEFINITION AM889471  
ACCESSION AM889471  
VERSION AM889471.1 GI:8053676  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 342)  
AUTHORS Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,  
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,  
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Bala,G.S., Simpson,D.H.,  
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare  
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and  
Simpson,A.J.  
TITLE Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL MEDLINE 2020263  
COMMENT Laboratory of Cancer Genetics  
Contact: Simpson A.J.G.  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=6t2-RC6-NT0029-280  
400-012-B08&tl3=2000-04-28&tl4=1)  
Seq primer: puc 18 forward  
High quality sequence stop: 342.

FEATURES  
Source Location/Qualifiers  
1. .342  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="NT0029"  
/dev\_stage="Adult"

/note="Organ: nervous\_tumor; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORSTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the pUC 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 83 a 98 c 105 g 56 t  
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 342;  
Best Local Similarity 100.0%; Pred. No. 43;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctgggccccctgg 708  
|||||  
Db 72 TGGGCTGCTGGGCCCCCTGG 52

RESULT 20  
A1823620 477 bp mRNA linear EST 21-DEC-1999  
LOCUS w171d07.x1 NCI\_CGAP\_Kid12 Homo sapiens CDNA clone IMAGE:2398765 3',  
DEFINITION mRNA sequence.  
ACCESSION A1823620  
VERSION A1823620.1 GI:5444291  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 477)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
Unpublished (1997)  
JOURNAL Contact: Robert Strausberg, Ph.D.  
COMMENT Email: cgaaps-remail.nih.gov  
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
DNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/ILNI at:  
www-bio.lnlnl.gov/bbrp/image/image.html  
Insert length: 811 Std Error: 0.00  
Seq primer: 400P from Gibco  
High quality sequence stop: 437.

FEATURES  
Source Location/Qualifiers  
1. .477  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="2398765"  
/clone\_lib="NCI\_CGAP\_Kid12"  
/tissue\_type="2 pooled tumors (clear cell type)"  
/lab\_host="DH10B"  
/note="Organ: kidney; Vector: pT73D-Pac (Pharmacia) with  
a modified polylinker; Site\_1: Not I; Site\_2: Eco RI;  
Plasmid DNA from the normalized library NCI\_CGAP\_Kid5 was  
prepared, and ss circles were made in vitro. Following HAP  
purification, this DNA was used as tracer in a subtractive  
hybridization reaction. The driver was PCR-amplified cDNAs  
from a pool of 5,000 clones made from the same library  
(cloneids 1323912-1325831, 1471368-1472903 and  
1492104-1493255). Subtraction by Bento Soares and M.  
Fatima Bonaldo."

BASE COUNT 104 a 94 c 180 g 97 t 2 others  
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 477;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctgggccccctgg 708  
|||||  
Db 475 TGGGCTGCTGGGCCCCCTGG 455

RESULT 21  
AA312871 480 bp mRNA linear EST 19-APR-1997  
LOCUS AA312871  
DEFINITION EST183529 Jurkat T-cells VI Homo sapiens CDNA 5' end, mRNA  
sequence.  
ACCESSION AA312871

VERSION AA312871.1 GI:1965219  
KEYWORDS EST.  
SOURCE Homo sapiens  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 480)  
AUTHORS Adams,M.D., Kerlavage,A.R., Fleischmann,R.D., Feldner,R.A., Bult  
C.J., Lee,N.H., Kinkness,E.F., Weinstock,K.G., Gocayne,J.D., White  
O., Sutton,G., Blake,J.A., Brandon,R.C., Man-ai,C., Clayton,R.A.,  
Cline,T.R., Cotton,M.D., Earle-Hughes,J., Fine,L.D., Fitzgerald  
L.M., Fitzhugh,W.M., Fritchman,J.L., Geoghagen,N.S., Glodde,A.  
Gneltun,C.L., Hanna,M.C., Hedblom,E., Hinkle,P.S., Jr., Kelley,J.M.,  
Kelley,J.C., Liu,L.-I., Marmaros,S.M., Merrick,J.M.,  
Moreno-Palauques,R.F., McDonald,L.A., Nguyen,D.T., Pelligrino,S.M.,  
Phillips,C.A., Ryder,S.E., Scott,J.L., Sauden,D.M., Shirley,R.,  
Small,K.V., Spriggs,T.A., Uteback,T.R., Weidman,J.F., Li,Y.,  
Bednarek,D.P., Cao,L., Cepeda,M.A., Coleman,T.A., Collins,E.J.,  
Ditke,D., Feng,D.-F., Fertle,A., Fischer,C., Hastings,G.A., He,W.M.,  
Hu,J.S., Greene,J.M., Gruber,J., Hudson,P., Kim,A.K., Kozak,D.L.,  
Kunsch,C., Hungjun,U., Li,H., Weissner,P.S., Olsen,H., Raymond,L.,  
Wei,Y.F., Wing,J., Xu,C., Yu,G.L., Ruben,S.M., Dillon,P.J., Fannon  
M.R., Rosen,C.A., Haseltine,W.A., Fields,C., Fraser,C.M. and  
Venter,J.C.  
TITLE Initial assessment of human gene diversity and expression patterns  
based upon 83 million nucleotides of cDNA sequence  
JOURNAL Nature 377 (6547 Suppl), 3-174 (1995)  
MEDLINE 96026280  
COMMENT Other\_ESTs: THC176037  
Contact: Kerlavage, AR  
Bioinformatics  
The Institute for Genomic Research  
9712 Medical Center Drive, Rockville, MD 20850 USA  
Tel: 3018699056  
Fax: 3018699423  
Email: arkerlav@ligr.org  
URL: arkerlav@ligr.org  
For clone availability, additional sequence and expression  
information related to this EST, please check the TIGR Human Gene  
Index (<http://www.tigr.org/cdb/hgi/hgi.html>)  
Seq primer: M13 Reverse.  
Location/Qualifiers  
FEATURES  
source 1..480  
/organism="Homo sapiens"  
/db\_xref="ATCC (Inhost):160191"  
/db\_xref="taxon:9606"  
/clone\_lib="Jurkat T-cells V1"  
/cell\_type="T-Lymphocyte"  
/note="Vector: pBluescript SK-; site\_1: EcoRI; site\_2:  
XhoI"

BASE COUNT 75 a 164 c 119 g 117 t 5 others  
ORIGIN  
Query Match 2.0%; Score 21; DB 9; Length 480;  
Best Local Similarity 100.0%; Pred. No. 44;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 688 tggggctgctggggcccccctgg 708  
DB 237 tggggctgctggggcccccctgg 257  
RESULT 22  
LOCUS A1126122 482 bp mRNA linear EST 28-OCT-1998  
DEFINITION gq77b04.x1 Soares\_testis\_NHT Homo sapiens cDNA clone IMAGE:1735471  
ACCESSION A1126122  
VERSION A1126122.1 GI:3594636  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
REFERENCE 1 (bases 1 to 482)  
AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
cDNA Library Preparation: M. Bento Soares, Ph.D., M. Fatima Bonaldo  
Ph.D.  
cDNA Library Arrayed by: Greg Lennon, Ph.D.  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.llnl.gov/bbrp/image/image.html](http://www.bio.llnl.gov/bbrp/image/image.html)  
Insert Length: 723 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amerisham  
High quality sequence stop: 444.  
Location/Qualifiers  
FEATURES  
source 1..482  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_image="IMAGE:1735471"  
/clone\_lib="Soares\_testis\_NHT"  
/sex="male"  
/lab\_host="DH10B"  
/note="Vector: p7773D-Pac (Pharmacia) with a modified  
polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st strand cDNA  
was prepared from mRNA obtained from Clontech Laboratories  
Inc., and primed with a Not I - oligo(dT) primer [5'  
TGTTCCATGTCGAGTGAGGAGCGCGCCGCCCAATTTTCTTTTCTTTT 3']  
Double-stranded cDNA was ligated to Eco RI adaptors  
(Pharmacia), digested with Not I and cloned into the Not I  
and Eco RI sites of the modified p7773 vector. Library  
went through one round of normalization to Cot5, and was  
constructed by Bento Soares and M. Fatima Bonaldo."



Email: est@watson.wustl.edu  
This clone is available royalty-free through LNL; contact the  
IMAGE Consortium (infoimage.lnl.gov) for further information.  
Insert length: 324 Std Error: 0.00  
Seq primer: -41m13 fwd. ET from Amersham  
High quality sequence stop: 471.

## FEATURES

Source

1. .545  
/organism="Homo sapiens"  
/db\_xref="Gene:5940824"  
/db\_xref="taxon:9606"  
/clone\_id="IMAGE:740877"  
/clone\_lib="Soares ovary tumor NDHOT"  
/sex="Female"  
/tissue\_type="ovarian tumor"  
/lab\_host="DH10B (ampicillin resistant)"  
/note="Organ: ovary; Vector: pT73D (Pharmacia) with a  
modified polylinker; Site\_1: Not I; Site\_2: Eco RI; 1st  
strand cDNA was primed with a Not I - oligo(dT) primer [5'  
TGTACCAATCTGAGTGGAGCGCGCGTGTGTGTGTGTGTGTGTGTGTGT  
3'],  
double-stranded cDNA was size selected, ligated to Eco RI  
adapters (Pharmacia), digested with Not I and cloned into  
the Not I and Eco RI sites of a modified pT73 vector  
(Pharmacia). Library constructed by Bento Soares and  
M. Palma Bonaldo."

BASE COUNT 120 a 117 c 204 g 103 t 1 others  
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 545;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggctgctggggccctgg 708  
|||||  
Db 468 TGGGCTCTGTGGCCCTGG 448

RESULT 24  
AL523655/c  
LOCUS  
DEFINITION AL523655 LTI\_NFL003\_NBC3 Homo sapiens cDNA clone CS0DC004YD06 3  
VERSION  
ACCESSION AL523655  
KEYWORDS  
SOURCE human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 572)  
Li, W. B., Gruber, C., Jesse, J. and Polayes, D.  
Full-length cDNA libraries and normalization  
Unpublished (2001)  
JOURNAL  
Contact: Genoscope  
Genoscope - Centre National de Sequencage  
BP 191 91006 Evry cedex - France  
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.  
FEATURES  
Source  
1. .572  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="CS0DC004YD06"  
/clone\_lib="LTI\_NFL003\_NBC3"  
/sex="male"  
/tissue\_type="neuroblastoma cells"  
/lab\_host="DH10B"  
/note="Organ: brain; Vector: pCMVSPORT 6; 1st strand cDNA  
was primed with a NotI-oliigo(dT) primer. Five prime end  
enriched, double-stranded cDNA was digested with Not I and  
cloned into the Not I and Eco RV sites of the pCMVSPORT 6  
vector. Library was normalized. Library was constructed  
by Life Technologies. Contact : Feng Liang Life

Technologies, a division of Invitrogen 9800 Medical Center  
Drive Rockville, Maryland 20850, USA Fax : (1) 301 610  
8371 Email : fliang@lifetech.com URL :  
http://fulllength.invitrogen.com"

BASE COUNT 134 a 134 c 191 g 86 t 27 others  
ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 572;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggctgctggggccctgg 708  
|||||  
Db 330 TGGGCTCTGTGGCCCTGG 310

RESULT 25  
BF810986  
LOCUS  
DEFINITION BF810986 585 bp mRNA linear EST 12-JAN-2001  
CM2-C10179-181100-528-F10 C10179 Homo sapiens cDNA, mRNA sequence.  
ACCESSION  
VERSION BF810986.1 GI:12139975  
KEYWORDS  
SOURCE human.  
ORGANISM  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
1 (bases 1 to 585)  
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M. R.,  
Nagai, M. A., da Silva, W. Jr., Zago, M. A., Bordin, S., Costa, F. F.,  
Goldman, G. H., Carvalho, A. F., Matsukuma, A., Bala, G. S., Simpson, D. H.,  
Brunstein, A., de Oliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare,  
M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and  
Simpson, A. J.  
Shotgun sequencing of the human transcriptome with ORF expressed  
sequence tags  
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)  
JOURNAL  
MEDLINE  
20202663  
Contact: Simpson A.J.G.  
Laboratory of Cancer Genetics  
Ludwig Institute for Cancer Research  
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,  
Brazil  
Tel: +55-11-2704922  
Fax: +55-11-2707001  
Email: asimpson@ludwig.org.br  
This sequence was derived from the FAPESP/LICR Human Cancer Genome  
Project. This entry can be seen in the following URL  
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&t2=CM2-C10179-  
181100-528-F10&t3=2000-11-18&t4=1)  
Seq primer: puc 18 forward  
High quality sequence start: 81  
High quality sequence stop: 285.

## FEATURES

Source

1. .585  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone\_lib="C10179"  
/dev\_stage="Adult"  
/note="Organ: colon; Vector: puc18; Site\_1: SmaI;  
Site\_2: SmaI; A mini-library was made by cloning products  
derived from ORESTES PCR (U.S. Letters Patent application  
No. 196,716 - Ludwig Institute for Cancer Research)  
profiles into the puc 18 vector. Reverse transcription of  
tissue mRNA and cDNA amplification were performed under  
low stringency conditions."  
BASE COUNT 92 a 189 c 173 g 131 t  
ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 585;  
Best Local Similarity 100.0%; Pred. No. 45;

Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0:

OY 688 tggggctgctggccctctg 708  
|||||  
Db 178 TGGGGCTGCTGGCCCCCTGG 198

RESULT 26  
A1264358 636 bp mRNA linear EST 27-JAN-1999  
LOCUS q109f04.x1 Soares NHMPL SI Homo sapiens cDNA clone IMAGE:1855999  
DEFINITION 3' similar to TR:O42154 O42154 GLUCOSE-6-PHOSPHATASE ; mRNA  
sequence.  
ACCESSION A1264358  
VERSION A1264358.1 GI:3872561  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 636)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
This clone is available royalty-free through LNL ; contact the  
IMAGE Consortium (info@image.lnl.gov) for further information.  
Insert length: 720 Std Error: 0.00  
Seq primer: -400p from G1bco  
High quality sequence stop: 399.  
FEATURES  
source  
1. 636  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:1855999"  
/clone\_1lb="Soares\_NHMPL\_SI"  
/tissue\_type="Pooled human melanocyte, fetal heart, and  
pregnant uterus"  
/lab\_host="DH10B"  
/note="Organ: mixed (see below); Vector: pT73D-Pac  
(Pharmacia) with a modified polylinker; Site: 1: Not I;  
Site: 2: Eco RI. Equal amounts of plasmid DNA from three  
normalized libraries (melanocyte 2MBH, pregnant uterus  
NBH9, and fetal heart NBH19W) were mixed, and ss circles  
were made in vitro. Following HAP purification, this DNA  
was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from pools of  
5,000 clones made from the same 3 libraries. The pools  
consisted of I.M.A.G.E. clones 260232-265223,  
340488-345479, and 484488-489479."

BASE COUNT 138 a 150 c 228 g 116 t 4 others

ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 636;  
Best Local Similarity 100.0%; Pred. No. 45;  
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

OY 688 tggggctgctggccctctg 708  
|||||  
Db 461 TGGGGCTGCTGGCCCCCTGG 441

RESULT 27  
A1669655 649 bp mRNA linear EST 17-DEC-1999  
LOCUS wc12a05.x1 NCI-CGAP\_Pr28 Homo sapiens cDNA clone IMAGE:2314928 3'  
DEFINITION similar to TR:O42154 O42154 GLUCOSE-6-PHOSPHATASE ; mRNA sequence.  
ACCESSION A1669655  
VERSION A1669655.1 GI:4834429  
KEYWORDS EST.

SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 649)  
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.  
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index  
JOURNAL Unpublished (1997)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: Michael J. Brownstein, M.D., Ph.D., Michael R.  
Emmert-Buck, M.D., Ph.D.  
CDNA Library Preparation: M. Bento Soares, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.  
DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. consortium/LNL at:  
www.bio.lnl.gov/bdrp/image/image.html  
Insert Length: 768 Std Error: 0.00  
Seq primer: -400p from G1bco  
High quality sequence stop: 454.  
FEATURES  
source  
1. 649  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:2314928"  
/clone\_1lb="NCI-CGAP\_Pr28"  
/sex="male"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/note="Organ: prostate; Vector: pT73D-Pac (Pharmacia)  
with a modified polylinker; Plasmid DNA from the  
normalized library NCI-CGAP\_Pr22 was prepared, and ss  
circles were made in vitro. Following HAP purification,  
this DNA was used as tracer in a subtractive hybridization  
reaction. The driver was PCR-amplified cDNAs from a pool  
of 5,000 clones made from the same library (cloneIDs  
985608-986759, 1101192-1101959, and 1217928-1220615).  
Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT 141 a 154 c 230 g 117 t 7 others

ORIGIN

Query Match 2.0%; Score 21; DB 9; Length 649;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 21: Conservative 0: Mismatches 0: Indels 0: Gaps 0;

OY 688 tggggctgctggccctctg 708  
|||||  
Db 468 TGGGGCTGCTGGCCCCCTGG 448

RESULT 28  
BM006189 650 bp mRNA linear EST 30-OCT-2001  
LOCUS 60361401f1 NIH\_MGC\_100 Homo sapiens cDNA clone IMAGE:5433602 5',  
DEFINITION mRNA sequence.  
ACCESSION BM006189  
VERSION BM006189.1 GI:16520543  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 650)  
AUTHORS NIH-MGC http://mhc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-r@mail.nih.gov  
Tissue Procurement: CGAP (Stanford)  
CDNA Library Preparation: Ling Hong/Rubin Laboratory

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov> row: f column: 03  
Plate: LNCM1909  
High quality sequence stop: 650.

FEATURES  
source

1. .650  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:543502"  
/clone\_lib="NIH\_MGC\_100"  
/tissue\_type="hepatocellular carcinoma, cell line"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: liver; Vector: pORF7; Site.1: XhoI; Site.2:  
EcoRI; cDNA made by oligo-dT priming. Directionally cloned  
into EcoRI/XhoI sites using the following 5' adaptor:  
GGCAGCGAG(G). Size selected >500bp for average insert size  
1.8kb. Library constructed by Ling Hong in the laboratory  
of Gerald M. Rubin (University of California, Berkeley)  
using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
II RT (Life Technologies). Note: this is a NIH\_MGC  
Library."

BASE COUNT 128 a 234 c 149 g 139 t  
ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 650;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccttg 708  
|||||  
Db 162 TGGGGCTGCTGGGCCCTCG 182

## RESULT 29

BF725110 653 bp mRNA linear EST 05-JAN-2001  
LOCUS  
DEFINITION bx12c11.y1 Human Iris cDNA (un-normalized, unamplified): Bx Homo  
sapiens cDNA clone bx12c11 5', mRNA sequence.

ACCESSION BF725110  
VERSION BF725110.1 GI:12041021  
KEYWORDS  
SOURCE EST.

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 653)  
AUTHORS Wistow,G.J., Bernstein,S., Behal,A. and Smith,D.  
TITLE Mammalian: EST analysis and bioinformatics for ocular genomics  
JOURNALS Invest. Ophthalmol. Vis. Sci. 41 (2000) In press  
COMMENT Contact: Wistow G  
Section on Molecular Structure and Function  
National Eye Institute  
6/331, NIH, Bethesda, MD 20892-2740, USA  
Tel: 301 402 3452  
Fax: 301 496 0078  
Email: graeme@helix.nih.gov  
Plate: 12 row: c column: 11  
Seq primer: M13RPI reverse primer (ABI).

FEATURES  
source

1. .653  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="bx12c11"  
/clone\_lib="Human Iris cDNA (un-normalized, unamplified):  
BX"  
/tissue\_type="Iris"  
/dev\_stage="Adult"  
/lab\_host="EMDH10B"  
/note="Organ: Eye; Vector: pCMVSPORT6; Post-mortem iris

tissue was pooled from 10 individuals ranging in age from  
4-80 years and RNA was extracted. From this pooled sample  
an aliquot of 60ug of total RNA yielded 2.17ug of mRNA. A  
directionally cloned cDNA library in the pCMVSPORT6 vector  
was constructed at Life Technologies, essentially  
following the protocols of the Superscript Plasmid System  
full details of which are contained in the manufacturer's  
instruction manual (<http://www.lifetech.com/>). First  
strand synthesis was carried out using a Not I  
primer-adaptor [5'-TGACATGTTCTAGATCGGAGCGGCCG(T)15-3'  
]. Not I/Dint end inserts were cloned into the Not I/EcoR  
V sites in the vector. EST analysis was performed on the  
unamplified library at the NIH Intramural Sequencing  
Center (NISC)."

BASE COUNT 101 a 208 c 183 g 161 t  
ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 653;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 688 tggggctgctggggcccttg 708  
|||||  
Db 553 TGGGGCTGCTGGGCCCTCG 573

## RESULT 30

BG422683 683 bp mRNA linear EST 14-MAR-2001  
LOCUS  
DEFINITION 602449189P1 NIH\_MGC\_14 Homo sapiens cDNA clone IMAGE:4587551 5',  
mRNA sequence.

ACCESSION BG422683  
VERSION BG422683.1 GI:13329189  
KEYWORDS  
SOURCE EST.

## ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 683)  
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNALS Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: DCRD/DTP

cDNA Library Preparation: Ling Hong/Rubin Laboratory  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Incyte Genomics, Inc.  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Plate: LNCM1318 row: a column: 24  
High quality sequence stop: 664.

FEATURES  
source

1. .683  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:4587551"  
/clone\_lib="NIH\_MGC\_14"  
/tissue\_type="renal cell adenocarcinoma"  
/lab\_host="DH10B (phage-resistant)"  
/note="Organ: kidney; Vector: pORF7; Site.1: XhoI; Site.2:  
EcoRI; cDNA made by oligo-dT priming. Directionally  
cloned into EcoRI/XhoI sites using the following 5'  
adaptor: GGCAGCGAG(G). Size selected >500bp for average  
insert size 1.8kb. Library constructed by Ling Hong in  
the laboratory of Gerald M. Rubin (University of  
California, Berkeley) using ZAP-cDNA synthesis kit  
(Stratagene) and Superscript II RT (Life Technologies)."

BASE COUNT 134 a 236 c 161 g 152 t  
ORIGIN

Query Match 2.0%; Score 21; DB 10; Length 683;  
Best Local Similarity 100.0%; Pred. No. 46;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 688 tgggctgtgtggccccctgg 708  
|||||  
DB 199 tgggctgtgtggccccctgg 219

Search completed: June 19, 2002, 01:45:26  
Job time: 2007 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:17:49 ; Search time 202.93 Seconds  
(without alignments)  
8951.340 Million cell updates/sec

Title: US-09-852-845-1

Perfect score: 1058

Sequence: 1 cagcagagacgagatgtgc.....cacataaaacctgtgcag 1058

Scoring table: OLIGO\_NUC  
Gapop 60.0 , Gapext 60.0

Searched: 1736436 seqs, 858457221 residues

Word size : 0

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

N\_Geneseq\_032802.\*  
1: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1980.DAT:\*  
2: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1981.DAT:\*  
3: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1982.DAT:\*  
4: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1983.DAT:\*  
5: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1985.DAT:\*  
6: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1986.DAT:\*  
7: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1987.DAT:\*  
8: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*  
9: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1988.DAT:\*  
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11: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1990.DAT:\*  
12: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1991.DAT:\*  
13: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1992.DAT:\*  
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16: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1995.DAT:\*  
17: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA1996.DAT:\*  
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22: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001A.DAT:\*  
23: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2001B.DAT:\*  
24: /SIDSI/gcgdata/hold-geneseq/geneseqn-emb1/NA2002.DAT:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	886	83.7	1057 16	AAQ88758
2	886	83.7	1057 16	AAQ88758
3	886	83.7	1057 16	AAQ88758
4	886	83.7	1057 16	AAQ88758
5	886	83.7	1057 16	AAQ88758
6	886	83.7	1057 16	AAQ88758
7	886	83.7	1057 16	AAQ88758
8	886	83.7	1057 16	AAQ88758
9	886	83.7	1057 16	AAQ88758

10	28	2.6	618	16	AAQ0826
11	28	2.6	618	19	AAV32640
12	28	2.6	1317	16	AAQ00829
13	28	2.6	1317	19	AAV32636
14	24	2.3	24	16	AAQ93255
15	23	2.2	5148	22	AAQ46585
16	22	2.1	22	22	AAH22273
17	21	2.0	21	22	AAH22272
18	21	2.0	1153	21	AAAB6860
19	21	2.0	1447	21	AACT6846
20	21	2.0	1461	22	AAK52633
21	21	2.0	1569	22	AAH22958
22	21	2.0	1658	22	AAK51649
23	21	2.0	5808	22	AAI36023
24	21	2.0	5808	22	AAK69724
25	21	2.0	38348	22	AAK84953
26	20	1.9	4466	23	ABL17164
27	20	1.9	6361	23	ABL15756
28	20	1.9	38272	22	AAK84952
29	19	1.8	19	22	AAH22274
30	19	1.8	637	22	AAK87821
31	19	1.8	883	22	AAH23724
32	19	1.8	884	21	AAZ51624
33	19	1.8	1110	22	ABA20758
34	19	1.8	1210	22	AAH23725
35	19	1.8	1356	21	AACT6656
36	19	1.8	1389	19	AAV29992
37	19	1.8	1413	20	AAK59084
38	19	1.8	1516	22	AAZ28357
39	19	1.8	1622	17	AACT34592
40	19	1.8	1981	21	AAZ98207
41	19	1.8	2713	22	AAH23726
42	19	1.8	3086	22	AAZ27649
43	19	1.8	6114	20	AAH23727
44	19	1.8	6132	20	AAH23728
45	19	1.8	7898	20	AAK59080
46	19	1.8	7898	20	AAK59081
47	19	1.8	12286	22	AAK42019
48	19	1.8	12286	22	AAK89560
49	18	1.7	47	21	AAZ69360
50	18	1.7	107	22	ABA50988

#### ALIGNMENTS

RESULT 1  
AAQ88758  
ID AAQ88758 standard; CDNA: 1057 BP.  
XX  
XX  
AC AAQ88758;  
XX  
XX  
DT 21-NOV-1995 (first entry)  
XX  
XX  
DE ACT-4 cell surface receptor cDNA sequence.  
XX  
XX  
KW Cell surface receptor; ACT-4; T-lymphocyte; T-cell; immune system;  
RN ss.  
XX  
XX  
OS Homo sapiens.  
XX  
XX  
FH Key  
FT CDS 15..845 Location/Qualifiers  
FT FT /\*tag= a  
FT FT misc\_signal 15..86 /\*tag= b  
FT FT polyA-site 1042..1047 /\*tag= c  
FT FT  
FT FT  
PN WO9512673-A.  
XX PD 11-MAY-1995.  
XX

Mouse type-II memb  
Mouse OX40 extrace  
Plasmod PDC406/OX4  
OX40/Fc CDNA. Syn  
PCR primer 1 for h  
Tumour suppressor  
OX40 reverse PCR p  
OX40 forward PCR p  
Human secreted pro  
Human ORF2401  
Human polynucleoti  
Human phosphatase  
Human polynucleoti  
Human musculoskele  
Human immune/haema  
Drosophila melanog  
Human immune/haema  
OX40 hybridisation  
Human digestive sy  
Oligonucleotide #3  
Human membrane cha  
Human nervous syst  
Oligonucleotide #4  
Human ORF2211  
Human BY55 CDNA se  
Human activated ca  
Human BBSR PLP CDN  
NTT-11 nerve prot  
Human signal pepti  
Oligonucleotide #5  
DNA encoding human  
Human T-type volta  
Human activated ca  
Human activated ca  
Genomic sequence #  
Human histone deac  
Human map-related  
Human breast cell

PF 03-NOV-1994; 94WO-GB02415.  
 XX 03-NOV-1993; 93US-0147784.  
 XX (BECTON ) BECTON DICKINSON CO.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Buck DW, Engleman EG, Godfrey W;  
 XX MPI; 1995-185777/24.  
 DR P-PSDB; AAR74737.  
 XX  
 PT Isolated ACT-4 receptor from activated T-cells - also its ligands and  
 XX antibodies, useful for treating diseases of the immune system  
 PS  
 XX Claim 1; Fig. 5; 82pp; English.  
 CC This sequence encodes the full-length cell surface receptor ACT-4  
 CC isolated from activated CD4+ T-lymphocytes. The sequence may be  
 CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or  
 CC fragments, and antibodies may be used for the treatment of transplant  
 CC rejection, graft-versus-host disease, autoimmune disease, etc.  
 XX  
 SQ Sequence 1057 BP; 176 A; 390 C; 344 G; 147 T; 0 other;

Query Match 83.7%; Score 886; DB 16; Length 1057;  
 Best Local Similarity 99.8%; Pred. No. 0;  
 Matches 1056; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 1 cagcagaagacgaagatgctgctgggctcgcgcgtcggcgccggtcgtcgcgtc 60  
 Db 1 cagcagaagacgaagatgctgctgggctcgcgcgtcggcgccggtcgtcgcgtc 60  
 QY 61 tgcctcctcctggcgccggtcgtcgcgtcgcgcgtcgcgcgtcgcgcgtcgcgcgtc 120  
 Db 61 tgcctcctcctggcgccggtcgtcgcgtcgcgcgtcgcgcgtcgcgcgtcgcgcgtc 120  
 QY 121 acccagcagaacgacgctgctgcacagatgacggccagcagaagatgagtcgcgtc 180  
 Db 121 acccagcagaacgacgctgctgcacagatgacggccagcagaagatgagtcgcgtc 180  
 QY 181 ggcgcgcgtcccgagaacagctgtgcgcgtcgcgcgtcgcgcgtcgcgcgtcgcgcgtc 240  
 Db 181 ggcgcgcgtcccgagaacagctgtgcgcgtcgcgcgtcgcgcgtcgcgcgtcgcgcgtc 240  
 QY 241 tcagctcccaagcctgcaagccctgcaagctgcaagctgcaagctgcaagctgcaagctgca 300  
 Db 241 tcagctcccaagcctgcaagccctgcaagctgcaagctgcaagctgcaagctgcaagctgca 300  
 QY 301 agcagctgtagcagcgccacacagacagatctgcgcgtcgcgcgtcgcgcgtcgcgcgtc 360  
 Db 301 agcagctgtagcagcgccacacagacagatctgcgcgtcgcgcgtcgcgcgtcgcgcgtc 360  
 QY 361 tggacgagctcgaagcctgtagctgtagctgtagctgtagctgtagctgtagctgtagctgtag 420  
 Db 361 tggacgagctcgaagcctgtagctgtagctgtagctgtagctgtagctgtagctgtagctgtag 420  
 QY 421 ggcgaacaacgagcctgcaagccctggaacacacacacacacacacacacacacacacacacacac 480  
 Db 421 ggcgaacaacgagcctgcaagccctggaacacacacacacacacacacacacacacacacacacac 480  
 QY 481 agcgcgcagcagaatctgtagcagcaatctgtagagacagagaccccccagcagcagcagc 540  
 Db 481 agcgcgcagcagaatctgtagcagcaatctgtagagacagagaccccccagcagcagcagc 540  
 QY 541 cccagagagacccagggcccccgcagcagccacacacacacacacacacacacacacacacacacac 600  
 Db 541 cccagagagacccagggcccccgcagcagccacacacacacacacacacacacacacacacacacac 600  
 QY 601 ccagaaacctcacagagacccctcacccgcgcgtgtagagtcgcccgcggcgctgtagctg 660  
 Db 601 ccagaaacctcacagagacccctcacccgcgcgtgtagagtcgcccgcggcgctgtagctg 660

QY 661 ccgcacatcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 720  
 Db 661 ccgcacatcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 720  
 QY 721 cccctgtaacctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 780  
 Db 721 cccctgtaacctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 780  
 QY 781 gagcagattccgagcccccac 840  
 Db 781 gagcagattccgagcccccac 840  
 QY 841 agatctgagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 900  
 Db 841 agatctgagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 900  
 QY 901 gctcgtcgtgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 960  
 Db 901 gctcgtcgtgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 960  
 QY 961 ctgacacgttctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1020  
 Db 961 ctgacacgttctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1020  
 QY 1021 cctcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1080  
 Db 1021 cctcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1080  
 QY 1020 cctcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1057  
 Db 1020 cctcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtagcctgtag 1057

RESULT 2  
 AAT04048  
 ID AAT04048 standard; cDNA; 1057 BP.  
 XX  
 AC AAT04048;  
 XX  
 DT 05-MAR-1996 (first entry)  
 XX  
 DE ACT-4-h-1 receptor cDNA sequence.  
 XX  
 KW ACT-4; specific binding partner; sbd; B cells; lymphocyte; GVHD;  
 KW graft versus host disease; immune response; transplantation;  
 KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;  
 KW HTLV; human T lymphocyte virus; inflammatory bowel disease;  
 KW screening; identification; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT CDS 15..849  
 FT sig\_peptide /tag- a  
 FT mat\_peptide /product- ACT-4-h-1 receptor.  
 FT polyA\_site 87..846 /tag- b  
 FT 1042..1048 /tag- c  
 FT 1042..1048 /tag- d  
 XX  
 PN W09521915-A1.  
 XX  
 PD 17-AUG-1995.  
 XX  
 PF 06-FEB-1995; 95WO-GB00238.  
 XX  
 PR 10-FEB-1994; 94US-0195967.  
 XX  
 PA (GREAVES ) GREAVES C P.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX  
 PI Engleman EG, Godfrey W;  
 XX  
 DR MPI; 1995-293117/38.

QY	1	cagcagagacagagatctgctctggggctctcggccgctcgccgagccctctgctgagctc	60
Db	1	cagcagagagacagagatctgctctggggctctcggggctctcggccgctcgctgctgctc	60
QY	61	tgtctctctctgggctctgggctctgagacacgtgacgggctctcacctgtctggggagacact	120
Db	61	tgtctctctctgggctctgggctctgagacacgtgaggggctctcacctgtctggggagacact	120
QY	121	accccaagcaacagacacggctgtctctgcacagaaftgcagagccacgggcaacagggaatgtgtagccgct	180
Db	121	accccaagcaacagacacggctgtctctgcacagaaftgcagagccacagggaacagggaatgtgtagccgct	180
QY	181	gcaagcagctctcccaagaaacaggtgtgtccgctccgtctggggccggggctctctacaacagacgttg	240
Db	181	gcaagcagctctcccaagaaacaggtgtgtccgctccgtctggggccggggctctctacaacagacgttg	240
QY	241	tcagatctccaagccgtctgcaaaacccctgcagacbfgtgtgtaaacctcaagaaagtgggaagtgtagaggga	300
Db	241	tcagatctccaagccgtctgcaaaacccctgcagacbfgtgtgtaaacctcaagaaagtgggaagtgtagaggga	300
QY	301	agcagcctgtgtgacggtccacacacagagacacaaatctctgcacctctgcgggtcggggacaccaagccccc	360
Db	301	agcagcctgtgtgacggtccacacacagagacacaaatctctgcacctctgcgggtcggggacaccaagccccc	360
QY	361	tgggacagctataaagctctgggaattgtacctgtgtcccccctgcctccagggcaacttctccag	420
Db	361	tgggacagctataaagctctgggaattgtacctgtgtcccccctgcctccagggcaacttctccag	420
QY	421	ggcgaacaacagagcgtctgcaagccctctggagcacaactgtgactctgggtgggaagacacacccctgc	480
Db	421	ggcgaacaacagagcgtctgcaagccctctggagcacaactgtgactctgggtgggaagacacacccctgc	480
QY	481	agcccggtccagcaaatagctctggagcagaactctgttgagagacaggagaccccccaagccaagcagac	540
Db	481	agcccggtccagcaaatagctctggagcagaactctgttgagagacaggagaccccccaagccaagcagac	540
QY	541	cccacggagaaacccaagggcccccccggtccagggccacatctgtccaaagcccaactgtgaagccctggc	600
Db	541	cccacggagaaacccaagggcccccccggtccagggccacatctgtccaaagcccaactgtgaagccctggc	600
QY	601	ccaaagaaacctcaacagggaaacctctcaaacccgggcccgtgtgaggtgtcccccggggccgctgacgtctg	660
Db	601	ccaaagaaacctcaacagggaaacctctcaaacccgggcccgtgtgaggtgtcccccggggccgctgacgtctg	660
QY	661	ccggacatctctgggctctgggctctgtgtctggggctgcgtctggggcccccctctggccaatctctgtctg	720
Db	661	ccggacatctctgggctctgggctctgtgtctggggctgcgtctggggcccccctctggccaatctctgtctg	720

CC  
CIE ON 40 antigen wa





DR WPI: 2001-328791/34.  
XX  
PT New nucleic acids encoding polypeptides with expanded primary signalling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans  
PT  
XX  
PS Example 2: Fig 3; 43pp; English.  
XX  
CC The invention relates to novel primary signalling motifs containing a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. CC They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus-host disease, or metabolic/diopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBS) of primary and secondary CC signalling motifs. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates CC primary activation of the T cell receptor (TCR) complex. Secondary CC motifs impart secondary or co-stimulatory signalling capacity to a CC molecule in T cells.  
XX  
SQ Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;  
XX  
Query Match 7.8%; Score 83; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.3e-27;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 735 cggagggaccagagctgcccccgatgccacaagcccccggggagagcagtttcgg 794  
Db 6 cggagggaccagagctgcccccgatgccacaagcccccggggagagcagtttcgg 65  
OY 795 accccatccaagagagcagc 817  
Db 66 accccatccaagagagcagc 88  
RESULT 6  
AAH24543  
ID AAH24543 standard; DNA: 117 BP.  
XX  
AC AAH24543;  
XX  
DT 08-AUG-2001 (first entry)  
XX  
DE Human secondary signalling motif SB34 oligo F1340A.  
XX  
KW Human: anti-HIV; antiinflammatory; antiasthmatic; dermatological; antisickling; antipsoriatic; neuroprotective; immunosuppressive; antiidiabetic; cytostatic; HIV infection; inflammation; autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis; neurological disease; organ transplant rejection; diabetes; cancer; graft-versus-host disease; adaptor receptor protein; sequence block; SB: primary signalling motif; secondary signalling motif; ss.  
XX  
OS Homo sapiens.  
XX  
PN WO200132866-A2.  
XX  
PD 10-MAY-2001.  
XX  
PF 01-NOV-2000; 2000WO-GB04189.  
XX

PR 01-NOV-1999; 99GB-0025854.  
XX  
PA (CELL-) CELTREC CHIROSCIENCE LTD.  
XX  
PI Finney HM, Lawson ADG;  
XX  
DR WPI: 2001-328790/34.  
XX  
XX  
PT Novel polynucleotide encoding adaptor receptor protein useful for treating human immunodeficiency virus (HIV) infection, asthma, cystic fibrosis, multiple sclerosis, organ transplant rejection, diabetes and cancer  
PT  
XX  
PS Example 3: Fig 3; 52pp; English.  
XX  
CC The invention relates to a novel nucleic acid encoding an adaptor receptor protein comprising an extracellular ligand-binding domain, a transmembrane domain and an intracellular signalling domain. The CC intracellular signalling domain comprises the cytoplasmic portion of at least one adaptor protein, and the extracellular ligand-binding domain is not CD8 or a major histocompatibility complex (MHC) class I protein. CC The adaptor receptor protein and the nucleic acid encoding it are useful in therapy. They are useful in the manufacture of a medicament for the CC treatment or prevention of disease in humans and animals. They are useful in the treatment of infectious diseases (e.g. HIV infection), CC inflammatory and autoimmune diseases (e.g. asthma and eczema), CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia), CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection, graft-versus-host CC disease and metabolic/diopathic diseases such as diabetes and cancer. CC The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBS) of primary and secondary CC signalling motifs. Primary signalling motifs transduce either a CC stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary signalling motifs impart CC secondary or co-stimulatory signalling capacity to a molecule in T CC cells. Primary and secondary signalling motifs may be used as components of the adaptor receptor protein of the invention.  
XX  
SQ Sequence 117 BP; 25 A; 45 C; 36 G; 11 T; 0 other;  
XX  
Query Match 7.8%; Score 83; DB 22; Length 117;  
Best Local Similarity 100.0%; Pred. No. 2.3e-27;  
Matches 83; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 735 cggagggaccagagctgcccccgatgccacaagcccccggggagagcagtttcgg 794  
Db 6 cggagggaccagagctgcccccgatgccacaagcccccggggagagcagtttcgg 65  
OY 795 accccatccaagagagcagc 817  
Db 66 accccatccaagagagcagc 88  
RESULT 7  
AAH24887/C  
ID AAH24887 standard; DNA: 117 BP.  
XX  
AC AAH24887;  
XX  
DT 22-AUG-2001 (first entry)  
XX  
DE Oligonucleotide for a secondary signalling motif.  
XX  
KW Stimulatory primary signalling motif; immune cell; signal transduction; chimeric receptor; inflammatory disease; autoimmune disease; asthma; eczema; congenital disease; cystic fibrosis; sickle cell anaemia; dermatological disease; psoriasis; neurological disease; multiple sclerosis; transplant-related disease; metabolic disease; organ transplant rejection; graft versus host disease; idiopathic disease; diabetes; cancer; ss.  
XX

OS	Synthetic.
XX	WO200132709-A2.
XX	10-MAY-2001.
XX	01-NOV-2000; 2000WO-GB04183.
XX	01-NOV-1999; 99GB-0025848.
XX	(CELL-) CELLTech CHIROSCIENCE LTD.
XX	Finney HM, Lawson ADG;
XX	WPI: 2001-389718/41.
XX	Novel cytoplasmic signalling protein and chimeric receptor protein, useful for treating HIV infection, asthma, eczema, psoriasis, multiple sclerosis, contain non-natural stimulatory primary signalling motif -
XX	Example 2; Fig 3; 45pp; English.
XX	Oligonucleotides AAH24886-87 were used to construct DNA encoding
XX	secondary signalling sequences. The specification describes stimulatory
XX	primary signalling motifs. Primary motifs are efficient at at
XX	mediating immune cell signal transduction, particularly when
XX	incorporated in an intracellular signalling domain of a chimeric
XX	receptor. The primary signalling motif can be combined in any way so
XX	as to achieve the desired level of activation (or inhibition) of a
XX	number of secondary messenger cascades. The signalling motifs are useful
XX	in therapy and in the manufacture of medicament for treating or
XX	preventing disease in humans or animals. They are useful for treating
XX	human patients suffering from infectious diseases e.g. human
XX	immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases
XX	such as asthma and eczema, congenital diseases e.g. cystic fibrosis,
XX	sickle cell anemia, dermatological diseases e.g. psoriasis, neurological
XX	diseases e.g. multiple sclerosis, transplant-related disease e.g. organ
XX	transplant rejection, graft versus host disease, metabolic/idiopathic
XX	disease e.g. diabetes, and cancer.
XX	Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
XX	Query Match 7.4%; Score 78; DB 22; Length 117;
XX	Best Local Similarity 100.0%; Pred. NO. 4e-25; Indels 0; Gaps 0
XX	Matches 78; Conservative 0; Mismatches 0;
QY	768 aagcccccgggggagagcagtlccggagaccccatcacaagagagagcagccgacccac 827
DB	83 AAGCCCCCGGGGGAGAGCGAGTTCCGACGCCCATCTCAGAGAGAGAGCGCCGACCCAC 24
QY	828 tccaccctggccaagatc 845
DB	23 TCCACCTGTGGCCAGATC 6
XX	AAH24478/C
XX	AAH24478 standard; DNA; 117 BP.
XX	AAH24478;
XX	07-AUG-2001 (first entry)
XX	Human secondary signalling motif SB34 oligo F1340B.
XX	Human; primary signalling motif; sequence block; SB; immunosuppressive;
XX	secondary signalling sequence; antimicrobial; antiinflammatory;
XX	dermatological; neuroprotective; cytostatic; anti-HIV; antisthmatic;
XX	antiskink; antiparasitic; antidiabetic; gene therapy; diabetes;
XX	immune cell signal transduction; infection; inflammation; cancer;
XX	autoimmune disease; congenital disease; psoriasis; neurological disease;
XX	organ transplant rejection; ss.

XX	Homo sapiens.
XO	
XX	WO200132867-A1.
PN	
XX	10-MAY-2001.
PD	
XX	01-NOV-2000; 2000WO-GB04193.
PF	
XX	01-NOV-1999; 99GB-0025853.
PR	
XX	(CELL-) CELLTECH CHIROSCIENCE LTD.
PA	
XX	Finney HM, Lawson ADG;
PI	
DR	WPI. 2001-328791/34.
XX	
XX	New nucleic acids encoding polypeptides with expanded primary signalling motifs, for use in gene therapy, particularly for treating or preventing infections, inflammations or autoimmune diseases in humans
PT	-
PS	
XX	Example 2; Fig 3; 43pp; English.
CC	
CC	The invention relates to novel primary signalling motifs containing a consensus amino acid sequence. These motifs are extremely efficient at mediating immune cell signal transduction, particularly when incorporated into an intracellular signalling domain of a chimeric receptor. Nucleic acids that encode, and polypeptides that contain, these primary signalling motifs are useful in medicine and research. They are useful in therapy, or in the manufacture of a medicament for treating or preventing disease in humans or in animals. These diseases include infections (e.g. HIV (human immunodeficiency virus) infection), inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological disorders (e.g. psoriasis), neurological diseases (e.g. multiple sclerosis), organ transplant rejection or graft-versus-host disease, or metabolic/diopathic diseases (e.g. diabetes or cancer). The present sequence is one of a large number of oligonucleotides used in the construction of sequence blocks (SBS) of primary and secondary signalling motifs. Primary signalling motifs are sequences that transduce either a stimulatory or an inhibitory signal, which regulates primary activation of the T cell receptor (TCR) complex. Secondary motifs impart secondary or co-stimulatory signalling capacity to a molecule in T cells.
CC	
XX	Sequence 117 BP; 11 A; 35 C; 45 G; 26 T; 0 other;
SQ	
	Query Match                7.4%; Score 78; DB 22; Length 117; Best Local Similarity     100.0%; Pred. No. 4e-25; Matches    78; Conservative    0; Mismatches    0; Indels    0; Gaps    0;
QY	768 aagcccccctggyggagcagtccggaccccccatccaaggagcgacgcgccacc 827       DB    83 AAGCCCCCTGGGGGAGCGAGTTTCCGGACCCCATCACAAGAGGACGACGCCCCAC 24 
QY	828 tcacccctggcgcaagatc 845 
DB	23 TTCACCCTGGCCAAGATC 6
RESULT    9	
ID    AAH24544/C	
XX    AAH24544 standard; DNA; 117 BP.	
XX    AAH24544;	
AC    08-AUG-2001 (first entry)	
DT    08-AUG-2001 (first entry)	
DE    Human secondary signalling motif SB34 oligo F1340B.	
XX    Human; anti-HIV; antiinflammatory; antistigmatic; dermatological;	



```
XX 22-JUN-1995; 95US-0494574.
XX 23-JUL-1993; 93US-0097827.
PR 22-JUN-1995; 95US-0494574.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
DR WPI: 1998-427099/36.
DR P-PSDB; AAW48977.
XX
PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
PT production and binding assays for OX-40 and homologues
XX
PS Example 1; Col 31-32; 26pp; English.
XX
CC The present sequence represents the mouse OX40 extracellular domain
CC encoding cDNA. The extracellular domain of OX40 is its ligand of the
CC binding domain. The present cDNA was used in the construction of the
CC chimeric OX40/Fc cDNA (AAV32640). The invention claims for a murine
CC OX40-L cytokine (AAW48975) that binds to the OX40 murine T cell antigen.
CC The OX40-L protein is claimed to be useful for co-stimulation of
CC T-cell production and in binding assays for detecting OX40 or its
CC homologues. The OX40-L protein is also claimed to generate a TH-2
CC immune response.
XX
SQ Sequence 618 BP; 148 A; 187 C; 151 G; 132 T; 0 other;

Query Match 2.6%; Score 28; DB 19; Length 618;
Best Local Similarity 100.0%; Pred. No. 0.0079;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaccagcctgcaagcctgaccac 451
DB 404 acaccagcctgcaagcctgaccac 431

RESULT 12
AAV00829
ID AAV00829 standard; cDNA; 1317 BP.
XX
AC AAT00829;
XX
DT 30-MAR-1996 (first entry)
XX
DE Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.
XX
KW OX40: OX40-L; cytokine; cell surface molecule; plasmid;
KW pDC406/OX40/Fc*; membrane glycoprotein; ss.
XX
OS Synthetic.
XX
FH Key 1.1317
FT CDS /tag= a
XX
XX US5457035-A.
XX
XX 10-OCT-1995.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX 23-JUL-1993; 93US-0097827.
XX
XX 23-JUL-1993; 93US-0097827.
XX
PA (IMMV ) IMMUNEX CORP.
XX
PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX
XX WPI: 1995-357992/46.
XX
XX P-PSDB; AAR81882.
XX
DR
```

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XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors
PT and host cells, used to produce recombinant ligand used in e.g.
PT prim. T cell culture, to modulate immune response etc.
XX
PS Example 2; Column 35-38; 26pp; English.
XX
CC This plasmid encodes an OX40/Fc antibody fragment mutein protein,
CC and is used to express a soluble OX40/Fc mutein fusion protein for
CC use in detecting cDNA clones encoding a OX40 ligand. The Fc
CC fragment may be derived from human IgG1, and the plasmid may be
CC used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell
CC line. Culture supernatant was purified by affinity chromatography
CC and this was used, together with labeled goat anti-human IgG to
CC screen various cell lines.
XX
SQ Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 2.6%; Score 28; DB 16; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaccagcctgcaagcctgaccac 451
DB 404 acaccagcctgcaagcctgaccac 431

RESULT 13
AAV32636
ID AAV32636 standard; cDNA to mRNA; 1317 BP.
XX
AC AAV32636;
XX
DT 25-SEP-1998 (first entry)
XX
DE OX40/Fc cDNA.
XX
DE OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
KW chimeric; ss.
XX
KW OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;
XX
OS Synthetic.
OS Chimeric - Homo sapiens.
OS Chimeric - Mus sp.
XX
FH Key 1.1317
FT CDS /tag= b
XX
XX mISC_feature 1.618
XX /tag= a
XX /note= "encodes mouse OX40 extracellular domain"
XX mISC_feature 619..1314
XX /tag= b
XX /note= "encodes mutant Fc region of human IgG1"
XX mutation 673..675
XX /tag= c
XX /note= "Changed from CTC in wild-type to GCC in
XX mutant"
XX mutation 676..678
XX /tag= d
XX /note= "changed from CTG in wild-type to GAG in
XX mutant"
XX mutation 682..684
XX /tag= e
XX /note= "changed from GGA in wild-type to GCG in
XX mutant"
XX US5783665-A.
XX
XX 21-JUL-1998.
XX
XX 22-JUN-1995; 95US-0494574.
XX
PF
```

```
XX 23-JUL-1993; 93US-0097827.
PR 22-JUN-1995; 95US-0494574.
XX (IMMUNEX CORP.
PA Baum PR, Fanslow WC, Gayle RB, Goodwin RG;
XX WPI: 1998-427099/36.
DR P-PSDB: AAW48976.
XX
PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell
PT production and binding assays for OX-40 and homologues
XX
PS Example 2; Col 35-38; 26pp; English.
XX
CC The present sequence represents the OX40/FC cDNA which encodes a
CC fusion protein that contains the extracellular domain of mouse OX40
CC fused to the mutated FC region of the human IgG1 antibody. The
CC fusion protein was used for detecting cDNA clones encoding an OX40
CC ligand. The invention claims for a murine OX40-L cytokine (AAW48975)
CC that binds to the murine T cell antigen, OX40. The OX40-L protein
CC is claimed to be useful for co-stimulation of T-cell production and
CC in binding assays for detecting OX40 or its homologues. The OX40-L
CC protein is also claimed to generate a TH-2 immune response.
XX
SQ Sequence 1317 BP; 322 A; 417 C; 337 G; 241 T; 0 other;

Query Match 2.6%; Score 28; DB 19; Length 1317;
Best Local Similarity 100.0%; Pred. No. 0.0074;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 424 acaccagcgctgcaagccctgaccac 451
    |||||||
DB 404 acaacgagcctgcaagccctgaccac 431

RESULT 14
AAQ93255
ID AAQ93255 standard; DNA: 24 BP.
XX
AC AAQ93255;
XX
DT 21-DEC-1995 (first entry)
XX
DE PCR primer 1 for human OX-40 cDNA.
XX
KW Primer: human OX-40; PCR; ss.
XX
OS Synthetic.
XX
PN WO9521251-A.
XX
PD 10-AUG-1995.
XX
PF 06-FEB-1995; 95WO-GB00237.
XX
PR 04-FEB-1994; 94US-0192480.
XX
PA (WEIN/) WEINBERG A D.
PA (CANT-) CANTAB PHARM RES LTD.
PI Vandenbark AA, Weinberg AD;
XX
DR WPI: 1995-283771/37.
XX
PT Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
PT develop prods. for detection and therapy of conditions mediated by
PT activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
XX
PS Example; Page 50; 91pp; English.
XX
```

```
CC Antigen OX-40 is specifically expressed on the cell surface of
CC antigen activated T-cells, especially, for example, CD4+ T-cells.
CC A human cDNA encoding the human OX-40 homologue was cloned using
CC primers 1 and 2. Template DNA for PCR amplification to product the
CC human OX-40 cDNA can be extracted from the lambda GT11 cDNA library
CC from human activated T-lymphocytes produced by Clontech, Palo Alto,
CC California (Catalog No. HL10316).
XX
SQ Sequence 24 BP; 1 A; 5 C; 13 G; 5 T; 0 other;

Query Match 2.3%; Score 24; DB 16; Length 24;
Best Local Similarity 100.0%; Pred. No. 0.64;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 atgtcgctggggcgctgcgcgcgtg 38
    |||||||
DB 1 atgtcgctggggcgctgcgcgcgtg 24

RESULT 15
AAS46585
ID AAS46585 standard; DNA: 5148 BP.
XX
AC AAS46585;
XX
DT 18-DEC-2001 (first entry)
XX
DE Tumour suppressor gene derived chemically modified sequence #307.
XX
KW Human; tumour suppressor gene; oncogene; antitumour; cytostatic;
KW cancer; tumour; CpG dinucleotide; single-nucleotide polymorphism; SNP;
KW cytosine methylation; ds.
XX
OS Homo sapiens.
XX
PN WO200168912-A2.
XX
PD 20-SEP-2001.
XX
PR 15-MAR-2001; 2001WO-EP02955.
XX
PR 15-MAR-2000; 2000DE-1013847.
PR 06-APR-2000; 2000DE-1019058.
PR 07-APR-2000; 2000DE-1019173.
PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX
PA (EPIG-) EPIGENOMICS AG.
XX
PI Olek A, Piepenbrock C, Berlin K;
XX
DR WPI: 2001-602752/68.
XX
PT Fragments of chemically modified genes associated with tumour suppressor
PT genes and oncogenes, useful in designing primers and probes for
PT analysing diseases associated with cytosine methylation state e.g.
PT cancer
XX
PS Claim 1; SEQ ID No 307; 27pp; English.
XX
CC The invention relates to a nucleic acid comprising a sequence of 18
CC bases, of a segment of chemically pretreated DNA (CP DNA) e.g. with
CC bisulphite, of genes associated with tumour suppression and
CC oncogenes, having a sequence taken from 536 (actually 533 since
CC numbers 408, 458 and 500 are missing from the sequence listing) sequences
CC (Ss) and sequences complementary to (Ss). The nucleic acid may be a
CC peptide nucleic acid-oligonucleotide (PNA) of at least 9 nucleotides and may
CC form part of a set of probes for detecting the cytosine methylation state
CC and/or single nucleotide polymorphisms and also to be used in an
CC array for analysing diseases associated with CpG dinucleotides e.g.
CC cancers and tumours. The probes can also be used in a method for
CC ascertaining genetic and/or epigenetic parameters for the diagnosis
```

CC and/or therapy of existing diseases or the predisposition to specific  
CC diseases, by analysing cytosine methylations. The parameters may be  
CC compared to another set of genetic and/or epigenetic parameters, the  
CC differences serving as basis for diagnosis and/or prognosis events which  
CC are disadvantageous to patients. The present sequence is one of the  
CC 533 genomic sequences derived from tumour suppressor genes and  
CC oncogenes.  
CC Note: The sequence data for this patent did not form part  
CC of the printed specification, but was obtained in electronic  
CC format directly from WIPO at  
CC ftp.wipo.int/pub/published\_pct\_sequences.  
SQ Sequence 5148 BP; 871 A; 182 C; 1479 G; 2615 T; 1 other;

Query Match 2.2%; Score 23; DB 22; Length 5148;  
Best Local Similarity 100.0%; Pred. No. 1.1;  
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 agagacgagatgcgtgaggg 27  
|||||  
DB 4796 agagacgagatgcgtgaggg 4818

RESULT 16  
AAH22273/C  
ID AAH22273 standard; DNA; 22 BP.  
XX  
AC AAH22273;  
XX  
DT 21-AUG-2001 (first entry)  
XX  
DE OX40 reverse PCR primer SEQ ID NO:19.  
XX  
XX Human; differentially expressed gene; angiogenesis; diagnosis;  
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;  
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;  
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;  
KM neovascularisation; restenosis; hypertension; aneurysm; angina;  
KM myocardial infarction; chronic heart condition; osteoporosis;  
KM PCR primer; hybridisation; probe; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200132926-A2.  
PN  
PD 10-MAY-2001.  
XX  
XX 01-NOV-2000; 2000WO-US30051.  
PF  
XX 01-NOV-1999; 99US-0162699.  
PR 13-APR-2000; 2000US-0196802.  
PR 31-OCT-2000; 2000US-0703350.  
XX  
PA (CURA-) CURAGEN CORP.  
PA (GETH) GENENTECH INC.  
PI Mehrahan F, Gerritsen M, Rastelli L;  
PI  
XX WPI; 2001-291056/30.  
DR  
XX  
XX Differentially expressed genes involved in angiogenesis, useful for  
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis  
PT subsequent to balloon angioplasty -  
XX  
XX Example 19; Page 147; 182pp; English.  
XX  
XX The present invention describes differentially expressed genes involved  
CC in angiogenesis (I), and the polypeptides that encode them. (I) have  
CC cardiovascular activity, and can be used in the modulation of  
CC angiogenesis. The nucleic acids and polypeptides may be used in the  
CC prevention, diagnosis and treatment of diseases associated with

CC inappropriate angiogenesis. The polypeptides may also be used as antigens  
CC in the production of antibodies against them and in assays to identify  
CC modulators of their expression and activity. The antibodies and  
CC antagonists may also be used to down regulate expression and activity  
CC and modulate angiogenesis. The antibodies may also be used as diagnostic  
CC agents for detecting the presence of the polypeptides in samples.  
CC Disorders that may be prevented, diagnosed and/or treated by the above  
CC methods include, for example vascular tumours, proliferative tumours,  
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,  
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis  
CC associated with neovascularisation, restenosis subsequent to balloon  
CC angioplasty, scar tissue over production, peripheral vascular disease,  
CC hypertension, inflammatory vasculitides, Reynaud's disease and  
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,  
CC lymphangitis, lymphedema, wound healing and tissue repair, ischaemia  
CC reperfusion injury, angina, myocardial infarctions, chronic heart  
CC conditions, heart failure such as congestive heart failure, age-related  
CC macular degeneration and osteoporosis. AAH22255 to AAH22325 and AAB98322  
CC to AAB98325 represent sequence used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 22 BP; 6 A; 4 C; 7 G; 5 T; 0 other;

Query Match 2.1%; Score 22; DB 22; Length 22;  
Best Local Similarity 100.0%; Pred. No. 5.1;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1001 gcttacctatgcataacc 1022  
|||||  
DB 22 GCTTACCGTATGCCATGCAATACC 1

RESULT 17  
AAH22272  
ID AAH22272 standard; DNA; 21 BP.  
XX  
AC AAH22272;  
XX  
DT 21-AUG-2001 (first entry)  
XX  
DE OX40 forward PCR primer SEQ ID NO:18.  
XX  
XX Human; differentially expressed gene; angiogenesis; diagnosis;  
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;  
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;  
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;  
KM neovascularisation; restenosis; hypertension; aneurysm; angina;  
KM myocardial infarction; chronic heart condition; osteoporosis;  
KM PCR primer; hybridisation; probe; ss.  
XX  
OS Homo sapiens.  
OS Synthetic.  
XX WO200132926-A2.  
PN  
PD 10-MAY-2001.  
XX  
XX 01-NOV-2000; 2000WO-US30051.  
PF  
XX 01-NOV-1999; 99US-0162699.  
PR 13-APR-2000; 2000US-0196802.  
PR 31-OCT-2000; 2000US-0703350.  
XX  
PA (CURA-) CURAGEN CORP.  
PA (GETH) GENENTECH INC.  
PI Mehrahan F, Gerritsen M, Rastelli L;  
PI  
XX WPI; 2001-291056/30.  
DR  
XX  
XX Differentially expressed genes involved in angiogenesis, useful for  
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis

PT subsequent to balloon angioplasty -  
XX  
PS Example 19; Page 147; 182pp; English.  
XX  
CC The present invention describes differentially expressed genes involved  
CC in angiogenesis (I), and the polypeptides that encode them. (I) have  
CC cardiovascular activity, and can be used in the modulation of  
CC angiogenesis. The nucleic acids and polypeptides may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate angiogenesis. The polypeptides may also be used as antigens  
CC in the production of antibodies against them and in assays to identify  
CC modulators of their expression and activity. The antibodies and  
CC antagonists may also be used to down regulate expression and activity  
CC and modulate angiogenesis. The antibodies may also be used as diagnostic  
CC agents for detecting the presence of the polypeptides in samples.  
CC Disorders that may be prevented, diagnosed and/or treated by the above  
CC methods include, for example vascular tumours, proliferative tumours,  
CC proliferative vitreoretinopathy, Rheumatoid arthritis, Crohn's disease,  
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis  
CC associated with neovascularisation, restenosis subsequent to balloon  
CC angioplasty, scar tissue over production, peripheral vascular disease,  
CC hypertension, inflammatory vasculitides, Reynaud's disease and  
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,  
CC lymphangitis, lymphedema, wound healing and tissue repair, Ischaemia  
CC reperfusion injury, angina, myocardial infarctions, chronic heart  
CC conditions, heart failure such as congestive heart failure, age-related  
CC macular degeneration and osteoporosis. AAH2225 to AAH22325 and AAH98322  
CC to AAH98325 represent sequence used in the exemplification of the  
CC present invention.  
XX  
SQ Sequence 21 BP; 4 A; 8 C; 4 G; 5 T; 0 other;

Query Match 2.0%; Score 21; DB 22; Length 21;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 955 ccaactctgaccgtctctagg 975  
|||||  
DB 1 ccaactctgaccgtctctagg 21

RESULT 18  
AAA87680  
ID AAA87680 standard; cDNA; 1153 BP.  
XX  
AC AAA87680;  
DT 04-DEC-2000 (first entry)  
XX  
DE Human secreted protein gene 15 SEQ ID NO:25.  
XX  
KW Human; secreted protein; immunosuppressive; immunostimulant; nocrotropic;  
KW antiinflammatory; cardiant; vulnerrary; antituler; anticonvulsant;  
KW antiparkinsonian; neuroprotective; antiviral; antibacterial; cytostatic;  
KW antiparasitic; thrombolytic; anticoagulant; antiarteriosclerotic;  
KW gene therapy; vaccine; chemotaxis-modulator; angiogenesis-modulator;  
KW cancer; immune system disorder; hyperproliferative disorder; infection;  
KW cardiovascular disorder; neurological disease; wound healing;  
KW chromosome 17; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200043495-A2.  
PD 27-JUL-2000.  
PF 18-JAN-2000; 2000WO-US00903.  
PR 19-JAN-1999; 99US-0116330.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX

PT Rosen CA, Ruben SM, Edner R, Young PE, Ni J, Moore PA;  
PI Komatsoulis G, Birse CE;  
XX  
DR WPI: 2000-499225/44.  
XX  
PS P-PSDB: AAB25679.  
XX  
PT New isolated polynucleotide encoding a secreted protein useful for  
PT preventing, treating or ameliorating a medical condition -  
XX  
PS Claim 1; Page 386; 451pp; English.  
XX  
CC The polynucleotide sequences given in AAA87666 to AAA87708 encodes the  
CC human secreted proteins given in AAB25665 to AAB25755. Human secreted  
CC proteins have activities based on the tissues and cells the genes are  
CC expressed in. Examples of activities include: immunosuppressive;  
CC immunostimulant; antiinflammatory; cardiant; vulnerrary; antituler;  
CC nocrotropic; antiviral; anticonvulsant; antiparkinsonian; neuroprotective;  
CC antibacterial; antiparasitic; thrombolytic; anticoagulant;  
CC antiarteriosclerotic and cytostatic. The secreted proteins and their  
CC polynucleotides can be used in gene therapy and as vaccines,  
CC chemotaxis-modulators and angiogenesis-modulators. The human secreted  
CC proteins and polynucleotides can be used for diagnosing (the  
CC susceptibility to) a pathological condition by determining the presence  
CC or absence of a mutation in the polynucleotide or determining the  
CC presence or amount of expression of the protein. The polynucleotides and  
CC proteins can also be used in the treatment and diagnosis of cancer,  
CC diseases of the immune system, hyperproliferative disorders,  
CC cardiovascular disorders and neurological disease. They can also be used  
CC to promote wound healing and to fight infection. AAA87657 to AAA87665 and  
CC AAB25664 represent sequences used in the exemplification of the present  
CC invention.  
XX  
SQ Sequence 1153 BP; 241 A; 376 C; 279 G; 255 T; 2 other;

Query Match 2.0%; Score 21; DB 21; Length 1153;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 688 tggggctgctggggccctctgg 708  
|||||  
DB 638 tggggctgctggggccctctgg 658

RESULT 19  
AAC76846  
ID AAC76846 standard; cDNA; 1447 BP.  
XX  
AC AAC76846;  
DT 08-FEB-2001 (first entry)  
XX  
DE Human ORFX ORF2401 polynucleotide sequence SEQ ID NO:4801.  
XX  
KW Human; open reading frame; ORFX; detection; cytostatic; hepatotropic;  
KW vulnerrary; antiparasitic; antiparkinsonian; nocrotropic; neuroprotective;  
KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;  
KW immunostimulant; thrombolytic; coagulant; vasotrophic; antidiabetic;  
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;  
KW antiviral; antibacterial; antifungal; antirheumatic; antithyroid;  
KW antianaemic; gene therapy; cancer; proliferative disorder; hypertension;  
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;  
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;  
KW cholesterol ester storage; systemic lupus erythematosus; infection;  
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;  
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;  
KW bone damage; cartilage damage; antiinflammatory disease; coagulation;  
KW thrombosis; contraceptive; ss.  
XX  
XX Homo sapiens.  
OS  
XX  
PN WO200058473-A2.

```

PD 05-OCT-2000.
XX
XX 31-MAR-2000; 2000MO-US08621.
XX
PR 31-MAR-1999; 99US-0127607.
PR 02-APR-1999; 99US-0127636.
PR 05-APR-1999; 99US-0127728.
PR 30-MAR-2000; 2000US-0540763.
XX
XX (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M.
XX
DR WPI; 2000-602362/57.
DR P-PSDB; AAB42637.
XX
XX Novel nucleic acids and peptides derived from open reading frame X,
PT useful for treating e.g. cancers, proliferative disorders,
PT neurodegenerative disorders and cardiovascular disease -
XX
XX Claim 5; Page 3984-3985; 5507pp; English.
XX
XX AAC74446 to AAC7606 encode the proteins given in AAB40237 to AAB43397,
CC which represent the human ORF open reading frames 1 to 3161. The ORF
CC sequences have activities such as: cytostatic; hepatotropic; vulnery;
CC antiproliferative; antiparkinsonian; nootropic; neuroprotective;
CC osteoprotective; anticonvulsant; antiallergic; immunosuppressive;
CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
CC antidiabetic; hypotensive; dermatological; immunosuppressive;
CC antihypertensive; antianemic. The sequences can be used for determining
CC the presence of or predisposition to, or preventing or treating
CC pathological conditions associated with an ORF-associated disorder. The
CC nucleic acids can be used to express ORF proteins in gene therapy
CC vectors. The proteins and nucleic acids may be used to treat cancers,
CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
CC graft vs host disease, cardiovascular disease, diabetes mellitus,
CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX
XX Sequence 1447 BP; 250 A; 477 C; 376 G; 341 T; 3 other;
SQ

```

Query Match 2.0%; Score 21; DB 21; Length 1447;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 688 tggggctgctgggccccctgg 708
   ||||||||||||||||
DB 965 tggggctgctgggccccctgg 985

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RESULT 20  
AAK52633  
ID AAK52633 standard; cDNA; 1461 BP.  
XX  
AC AAK52633;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
XX Human polynucleotide SEQ ID NO 2162.  
DE  
XX  
XX Human: cytokine; cell proliferation; cell differentiation; gene therapy;  
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;  
KW tissue growth factor; immunomodulatory; cancer; leukaemia;  
KW nervous system disorder; arthritis; inflammation; ss.  
XX  
OS Homo sapiens.  
XX

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PN WO200157190-A2.
XX
XX 09-AUG-2001.
XX
XX 05-FEB-2001; 2001MO-US04098.
XX
XX 03-FEB-2000; 2000US-0496914.
XX
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi Y, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R.
XX
XX WPI; 2001-476283/51.
DR P-PSDB; AAM79500.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
PT useful in diagnosis and gene therapy -
XX
XX Claim 1; Page 4529; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAK80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM60020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
XX Sequence 1461 BP; 249 A; 487 C; 382 G; 343 T; 0 other;
SQ

```

Query Match 2.0%; Score 21; DB 22; Length 1461;  
Best Local Similarity 100.0%; Pred. No. 10;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 688 tggggctgctgggccccctgg 708
   ||||||||||||||||
DB 982 tggggctgctgggccccctgg 1002

```

RESULT 21  
AAH22958  
ID AAH22958 standard; cDNA; 1569 BP.  
XX  
AC AAH22958;  
XX  
DT 17-SEP-2001 (first entry)  
XX  
XX Human phosphatase (PP) encoding cDNA (clone ID 1269556CB1).  
DE  
XX  
XX Phosphatase: PP; Alzheimer's disease; Huntington's disease; human;  
KW immune disorder; cancer; nootropic; immunomodulatory; cytostatic;  
KW neuroprotective; anticonvulsant; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers





PD 02-AUG-2001.  
XX 17-JAN-2001; 2001WO-US01338.  
XX  
PR 31-JAN-2000; 2000US-0179065.  
PR 04-FEB-2000; 2000US-0180628.  
PR 24-FEB-2000; 2000US-0184664.  
PR 02-MAR-2000; 2000US-0186350.  
PR 16-MAR-2000; 2000US-0189874.  
PR 17-MAR-2000; 2000US-0190076.  
PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.  
PR 11-JUL-2000; 2000US-0217487.  
PR 11-JUL-2000; 2000US-0217496.  
PR 14-JUL-2000; 2000US-0218290.  
PR 26-JUL-2000; 2000US-0220963.  
PR 26-JUL-2000; 2000US-0220964.  
PR 14-AUG-2000; 2000US-0224518.  
PR 14-AUG-2000; 2000US-0224519.  
PR 14-AUG-2000; 2000US-0225213.  
PR 14-AUG-2000; 2000US-0225214.  
PR 14-AUG-2000; 2000US-0225266.  
PR 14-AUG-2000; 2000US-0225267.  
PR 14-AUG-2000; 2000US-0225268.  
PR 14-AUG-2000; 2000US-0225270.  
PR 14-AUG-2000; 2000US-0225447.  
PR 14-AUG-2000; 2000US-0225757.  
PR 14-AUG-2000; 2000US-0225758.  
PR 14-AUG-2000; 2000US-0225759.  
PR 18-AUG-2000; 2000US-0226279.  
PR 22-AUG-2000; 2000US-0226681.  
PR 22-AUG-2000; 2000US-0226868.  
PR 22-AUG-2000; 2000US-0227182.  
PR 23-AUG-2000; 2000US-0227009.  
PR 30-AUG-2000; 2000US-0228924.  
PR 01-SEP-2000; 2000US-0228287.  
PR 01-SEP-2000; 2000US-0229343.  
PR 01-SEP-2000; 2000US-0229344.  
PR 01-SEP-2000; 2000US-0229345.  
PR 05-SEP-2000; 2000US-0229509.  
PR 05-SEP-2000; 2000US-0229513.  
PR 06-SEP-2000; 2000US-0230437.  
PR 06-SEP-2000; 2000US-0230438.  
PR 08-SEP-2000; 2000US-0231242.  
PR 08-SEP-2000; 2000US-0231243.  
PR 08-SEP-2000; 2000US-0231244.  
PR 08-SEP-2000; 2000US-0231413.  
PR 08-SEP-2000; 2000US-0231414.  
PR 08-SEP-2000; 2000US-0232080.  
PR 08-SEP-2000; 2000US-0232081.  
PR 12-SEP-2000; 2000US-0231968.  
PR 12-SEP-2000; 2000US-0232397.  
PR 14-SEP-2000; 2000US-0232398.  
PR 14-SEP-2000; 2000US-0232399.  
PR 14-SEP-2000; 2000US-0232400.  
PR 14-SEP-2000; 2000US-0232401.  
PR 14-SEP-2000; 2000US-0233063.  
PR 14-SEP-2000; 2000US-0233064.  
PR 14-SEP-2000; 2000US-0233065.  
PR 21-SEP-2000; 2000US-0234223.  
PR 21-SEP-2000; 2000US-0234274.  
PR 25-SEP-2000; 2000US-0234997.  
PR 25-SEP-2000; 2000US-0234998.  
PR 26-SEP-2000; 2000US-0235484.  
PR 27-SEP-2000; 2000US-0235834.  
PR 27-SEP-2000; 2000US-0235836.  
PR 29-SEP-2000; 2000US-0236327.  
PR 29-SEP-2000; 2000US-0236367.  
  
PR 29-SEP-2000; 2000US-0236368.  
PR 29-SEP-2000; 2000US-0236369.  
PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241221.  
PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.  
PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0246474.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
PR 08-NOV-2000; 2000US-0246526.  
PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
PR 17-NOV-2000; 2000US-0249209.  
PR 17-NOV-2000; 2000US-0249210.  
PR 17-NOV-2000; 2000US-0249211.  
PR 17-NOV-2000; 2000US-0249212.  
PR 17-NOV-2000; 2000US-0249213.  
PR 17-NOV-2000; 2000US-0249214.  
PR 17-NOV-2000; 2000US-0249215.  
PR 17-NOV-2000; 2000US-0249216.  
PR 17-NOV-2000; 2000US-0249217.  
PR 17-NOV-2000; 2000US-0249218.  
PR 17-NOV-2000; 2000US-0249244.  
PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250391.  
PR 05-DEC-2000; 2000US-0251030.  
PR 05-DEC-2000; 2000US-0251988.  
PR 05-DEC-2000; 2000US-0256719.  
PR 06-DEC-2000; 2000US-0251479.  
PR 08-DEC-2000; 2000US-0251856.  
PR 08-DEC-2000; 2000US-0251858.  
PR 08-DEC-2000; 2000US-0251869.  
PR 08-DEC-2000; 2000US-0251989.  
PR 08-DEC-2000; 2000US-0251990.  
PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
  
(HUMA-) HUMAN GENOME SCI INC.  
PA Rosen CA, Barash SC, Ruben SM;  
XX  
XX  
PI  
XX  
DR WPI: 2001-451937/48.

```
XX Isolated polypeptide for treating, preventing and/or prognosing
PR disorders related to the musculoskeletal system including
PR musculoskeletal cancers and also for testing and detection e.g.
PR diagnosis -
PS
XX Example 2: SEQ ID NO 2388; 781bp + Sequence Listing; English.
XX
CC The invention relates to novel genes (AAL34669-AAL37666) and proteins
CC (ABB03087-ABB04109) associated with the musculoskeletal system useful
CC for preventing, treating or ameliorating medical conditions e.g. by
CC protein or gene therapy. The genes are isolated from a range of human
CC tissues disclosed in the specification. The nucleic acids, proteins,
CC antibodies and (ant)agonists are useful in the diagnosis, treatment
CC and prevention of: (a) cancer, e.g. breast and ovarian cancer and
CC other cancers of the adrenal gland, bone, bone marrow, breast,
CC gastrointestinal tract, liver, lung, or urogenital; (b) immune
CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis;
CC (c) cardiovascular disorders such as myocardial ischaemias; (d) wound
CC healing; (e) neurological diseases e.g. cerebral anoxia and epilepsy;
CC and (f) infectious diseases such as viral, bacterial, fungal and
CC parasitic infections.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pcl_sequences.
XX
SQ Sequence 5808 BP; 1521 A; 1464 C; 1655 G; 1168 T; 0 other;
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Query Match 2.0%; Score 21; DB 22; Length 5808;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 688 tggggctgctgggccccctgg 708  
|||||  
Db 471 TGGGGCTGCTGGGCCCTGG 451

RESULT 24  
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ID AAK69724 standard; DNA; 5808 BP.  
XX  
AC AAK69724;  
XX  
DT 06-NOV-2001 (first entry)  
XX  
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:24536.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
XX cytosolic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01354.  
XX  
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PR 30-JUN-2000; 2000US-0215135.  
PR 07-JUL-2000; 2000US-0216647.

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PR 14-AUG-2000; 2000US-0225757.  
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PR 22-AUG-2000; 2000US-0226681.  
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PR 23-AUG-2000; 2000US-0227182.  
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PR 29-SEP-2000; 2000US-0236368.  
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PR 29-SEP-2000; 2000US-0236370.  
PR 02-OCT-2000; 2000US-0236802.  
PR 02-OCT-2000; 2000US-0237037.  
PR 02-OCT-2000; 2000US-0237038.  
PR 02-OCT-2000; 2000US-0237039.  
PR 02-OCT-2000; 2000US-0237040.  
PR 13-OCT-2000; 2000US-0239935.  
PR 13-OCT-2000; 2000US-0239937.  
PR 20-OCT-2000; 2000US-0240960.  
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PR 20-OCT-2000; 2000US-0241785.  
PR 20-OCT-2000; 2000US-0241786.  
PR 20-OCT-2000; 2000US-0241787.  
PR 20-OCT-2000; 2000US-0241808.
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PR 20-OCT-2000; 2000US-0241809.  
PR 20-OCT-2000; 2000US-0241826.  
PR 01-NOV-2000; 2000US-0244617.  
PR 08-NOV-2000; 2000US-0244674.  
PR 08-NOV-2000; 2000US-0246475.  
PR 08-NOV-2000; 2000US-0246476.  
PR 08-NOV-2000; 2000US-0246477.  
PR 08-NOV-2000; 2000US-0246478.  
PR 08-NOV-2000; 2000US-0246523.  
PR 08-NOV-2000; 2000US-0246524.  
PR 08-NOV-2000; 2000US-0246525.  
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PR 08-NOV-2000; 2000US-0246527.  
PR 08-NOV-2000; 2000US-0246528.  
PR 08-NOV-2000; 2000US-0246532.  
PR 08-NOV-2000; 2000US-0246609.  
PR 08-NOV-2000; 2000US-0246610.  
PR 08-NOV-2000; 2000US-0246611.  
PR 08-NOV-2000; 2000US-0246613.  
PR 17-NOV-2000; 2000US-0249207.  
PR 17-NOV-2000; 2000US-0249208.  
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PR 17-NOV-2000; 2000US-0249215.  
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PR 17-NOV-2000; 2000US-0249245.  
PR 17-NOV-2000; 2000US-0249264.  
PR 17-NOV-2000; 2000US-0249265.  
PR 17-NOV-2000; 2000US-0249297.  
PR 17-NOV-2000; 2000US-0249299.  
PR 17-NOV-2000; 2000US-0249300.  
PR 01-DEC-2000; 2000US-0250160.  
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PR 05-DEC-2000; 2000US-0251030.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
XX  
XX (HUMA-) HUMAN GENOME SCI INC.  
XX  
XX Rosen CA, Barash SC, Ruben SM;  
PI  
XX WPI; 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
PT useful for preventing, diagnosing and/or treating cancers and  
PT metastasis -  
XX  
XX  
PS Disclosure; SEQ ID NO 24536; 3071pp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patients own production of (I). Additionally, (I)

CC polynucleotides may be used to produce the secreted (I), by inserting  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX  
SQ Sequence 5808 BP; 1168 A; 1655 C; 1464 G; 1521 T; 0 other;  
  
Query Match 2.0%; Score 21; DB 22; Length 5808;  
Best Local Similarity 100.0%; Pred. No. 8.9;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 688 tggggctgctggggccctgg 708  
DB 5338 tggggctgctggggccctgg 5358.  
  
RESULT 25  
AAK84953  
ID AAK84953 standard; DNA; 38348 BP.  
XX  
AC AAK84953;  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Human immune/hematopoietic antigen genomic sequence SEQ ID NO:39765.  
XX  
KW Human; immune; haematopoietic; immune/hematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
XX Homo sapiens.  
XX  
PN WO200157182-A2.  
XX  
PD 09-AUG-2001.  
XX  
PF 17-JAN-2001; 2001WO-US01354.  
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XX  
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PR 17-MAR-2000; 2000US-0190076.  
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PR 01-DEC-2000; 2000US-0250160.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-0259678.  
  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX Rosen CA, Barash SC, Ruben SM;  
XX WPI: 2001-483426/52.  
XX  
XX Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
XX useful for preventing, diagnosing and/or treating cancers and  
XX metastasis -  
XX  
XX  
XX Disclosure; SEQ ID NO 39765; 3071bp + Sequence Listing; English.  
XX  
XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
XX amino acid sequences given in AAM82170 to AAM91921. (I) have cytosolic  
XX activity, and can be used in gene therapy and vaccine production. (I)  
XX proteins and polynucleotides may be used in the prevention, diagnosis and  
XX treatment of diseases associated with inappropriate (I) expression. For  
XX example, they may be used to treat disorders associated with decreased  
XX expression by rectifying mutations or deletions in a patient's genome  
XX that affect the activity of (I) by expressing inactive proteins or to  
XX supplement the patient's own production of (I). Additionally, (I)  
XX polynucleotides may be used to produce the secreted (I), by inserting  
XX the nucleic acids into a host cell and culturing the cell to express the  
XX protein. (I) proteins and polynucleotides may be used to prevent,  
XX diagnose and treat immune/hematopoietic-related diseases, especially  
XX cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
XX to AAK87694 represent human immune/hematopoietic antigen genomic  
XX sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
XX represent sequences used in the exemplification of the present invention.  
XX  
XX Sequence 38348 BP; 9411 A; 7405 C; 8303 G; 13229 T; 0 other;  
  
Query Match 2.0%; Score 21; DB 22; Length 38348;  
Best Local Similarity 100.0%; Pred. No. 7.5;  
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 684 gtgcctggggctgctggccccc 704  
DB 34516 gtgcctggggctgctggccccc 34536

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RESULT 26
ABL17164
ID ABL17164 standard; DNA; 4466 BP.
XX
XX ABL17164;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster genomic polynucleotide SEQ ID NO 2965.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW pharmaceutical; gene; ds.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PA
XX
XX (PEKE ) PE CORP NY.
PI
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
DR
XX
XX WPI: 2001-656860/75.
PT
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS
XX
XX Claim 1: SEQ ID NO 2965; 21bp + Sequence Listing; English.
CC
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
CC
XX
XX Sequence 4466 BP; 1312 A; 945 C; 916 G; 1293 T; 0 other;

Query Match 1.9%; Score 20; DB 23; Length 4466;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 994 gctctgcttacctatgcc 1013
DB 186 gctctgcttacctatgcc 205

RESULT 27
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ID ABL15756 standard; cDNA; 6361 BP.
XX
XX ABL15756;
AC
XX
XX 26-MAR-2002 (first entry)
DT
XX
XX Drosophila melanogaster expressed polynucleotide SEQ ID NO 41750.
DE
XX
XX Drosophila: developmental biology; cell signalling; insecticide;
KW

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KW pharmaceutical; gene; ss.
XX
XX Drosophila melanogaster.
OS
XX
XX WO200171042-A2.
PN
XX
XX 27-SEP-2001.
PD
XX
XX 23-MAR-2001; 2001WO-US09231.
PF
XX
XX 23-MAR-2000; 2000US-191637P.
PR
XX
XX 11-JUL-2000; 2000US-0614150.
PA
XX
XX (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI: 2001-656860/75.
XX
XX P-PSDB; ABB71653.
DR
XX
XX New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
PS
XX
XX Claim 1: SEQ ID NO 41750; 21bp + Sequence Listing; English.
CC
XX
XX The invention relates to an isolated nucleic acid detection reagent
CC capable of detecting 1000 or more genes from Drosophila. The invention is
CC useful in developmental biology and in elucidating cell signalling and
CC cell-cell interactions in higher eukaryotes for the development of
CC insecticides, therapeutics and pharmaceutical drugs. The invention
CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
CC sequences (ABL01840-ABL16175) and the encoded proteins
CC (AB57737-AB572072).
CC The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
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XX Sequence 6361 BP; 1759 A; 1273 C; 1395 G; 1934 T; 0 other;

Query Match 1.9%; Score 20; DB 23; Length 6361;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 994 gctctgcttacctatgcc 1013
DB 5437 gctctgcttacctatgcc 5456

RESULT 28
AAK84952
ID AAK84952 standard; DNA; 38272 BP.
XX
XX AAK84952;
AC
XX
XX 07-NOV-2001 (first entry)
DT
XX
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:39764.
DE
XX
XX Human: immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW cytostatic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
OS
XX
XX WO200157182-A2.
PN
XX
XX 09-AUG-2001.
PD
XX
XX 17-JAN-2001; 2001WO-US01354.
PF
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XX 31-JAN-2000; 2000US-0179065.
PR
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XX 04-FEB-2000; 2000US-0180628.

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PR 24-FEB-2000; 2000US-0184664.  
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PR 17-MAR-2000; 2000US-0190076.  
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PR 08-DEC-2000; 2000US-0251989.  
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PR 11-DEC-2000; 2000US-0254097.  
PR 05-JAN-2001; 2001US-02559678.  
  
(HUMA-) HUMAN GENOME SCI INC.  
Rosen CA, Barash SC, Ruben SM;  
WPI; 2001-483426/52.  
Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
useful for preventing, diagnosing and/or treating cancers and  
metastasis -  
PS Disclosure; SEQ ID NO 39764; 3071pp + Sequence Listing; English.

XX AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
CC amino acid sequences given in AAK62170 to AAK91921. (I) have cytostatic  
CC activity, and can be used in gene therapy and vaccine production. (I)  
CC proteins and polynucleotides may be used in the prevention, diagnosis and  
CC treatment of diseases associated with inappropriate (I) expression. For  
CC example, they may be used to treat disorders associated with decreased  
CC expression by rectifying mutations or deletions in a patient's genome  
CC that affect the activity of (I) by expressing inactive proteins or to  
CC supplement the patient's own production of (I). Additionally, (I)  
CC polynucleotides may be used to produce the secreted (I), by inserting the  
CC the nucleic acids into a host cell and culturing the cell to express the  
CC protein. (I) proteins and polynucleotides may be used to prevent,  
CC diagnose and treat immune/hematopoietic-related diseases, especially  
CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
CC to AAK87694 represent human immune/hematopoietic antigen genomic  
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
CC represent sequences used in the exemplification of the present invention.  
XX

SQ Sequence 38272 BP; 9399 A; 7384 C; 8269 G; 13220 T; 0 other;

Query Match 1.9%; Score 20; DB 22; Length 38272;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 684 gtgctgggctgctggcc 703  
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DB 34448 gtgctgggctgctggcc 34467

RESULT 29  
AAH22274  
ID AAH22274 standard; DNA; 19 BP.

XX AAH22274;  
XX  
DT 21-AUG-2001 (first entry)

DE OX40 hybridisation probe SEQ ID NO:20.

XX Human; differentially expressed gene; angiogenesis; diagnosis;  
KM angiogenic disorder; wound healing; cancer; cardiovascular; psoriasis;  
KM vascular tumour; proliferative tumour; proliferative vitreoretinopathy;  
KM rheumatoid arthritis; Crohn's disease; atherosclerosis; endometriosis;  
KM neovascularisation; restenosis; hypertension; aneurysm; angina;  
KM myocardial infarction; chronic heart condition; osteoporosis;  
KM PCR primer; hybridisation; probe; ss.

XX Homo sapiens.  
OS Synthetic.

XX WO200132926-A2.

XX 10-MAY-2001.

PD 01-NOV-2000; 2000MO-US30051.

XX 01-NOV-1999; 99US-0162699.

PR 13-APR-2000; 2000US-0196802.

PR 31-OCT-2000; 2000US-0703350.

XX (CURA-) CURAGEN CORP.

PA (GENTH) GENENTECH INC.

XX Mehraban F, Gerltzen M, Rastelli L;

DR WPI; 2001-291056/30.

XX Differentially expressed genes involved in angiogenesis, useful for  
PT treating e.g. vascular tumors, atherosclerosis and/or restenosis  
PT subsequent to balloon angioplasty -  
XX

PS Example 19; Page 147; 182pp; English.

XX The present invention describes differentially expressed genes involved  
CC in angiogenesis (I), and the polypeptides that encode them. (I) have  
CC cardiovascular activity, and can be used in the modulation of  
CC angiogenesis. The nucleic acids and polypeptides may be used in the  
CC prevention, diagnosis and treatment of diseases associated with  
CC inappropriate angiogenesis. The polypeptides may also be used as antigens  
CC in the production of antibodies against them and in assays to identify  
CC modulators of their expression and activity. The antibodies and  
CC antagonists may also be used to down regulate expression and activity  
CC and modulate angiogenesis. The antibodies may also be used as diagnostic  
CC agents for detecting the presence of the polypeptides in samples.  
CC Disorders that may be prevented, diagnosed and/or treated by the above  
CC methods include, for example vascular tumours, proliferative tumours,  
CC proliferative vitreoretinopathy, rheumatoid arthritis, Crohn's disease,  
CC atherosclerosis, ovarian hyperstimulation, psoriasis, endometriosis  
CC associated with neovascularisation, restenosis subsequent to balloon  
CC angioplasty, scar tissue over production, peripheral vascular disease,  
CC hypertension, inflammatory vasculitides, Reynaud's disease and  
CC Reynaud's phenomenon, aneurysms, arterial restenosis, thrombophlebitis,  
CC lymphangitis, lymphedema, wound healing and tissue repair, ischemia  
CC reperfusion injury, angina, myocardial infarctions, chronic heart  
CC conditions, heart failure such as congestive heart failure, age-related  
CC macular degeneration and osteoporosis. AAH22255 to AAH23325 and AAB98322  
CC to AAB98325 represent sequence used in the exemplification of the  
CC present invention.  
XX

SQ Sequence 19 BP; 1 A; 8 C; 6 G; 4 T; 0 other;

Query Match 1.8%; Score 19; DB 22; Length 19;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 978 ccgatgctgctccgcgct 996  
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DB 1 ccgatgctgctccgcgct 19

RESULT 30  
AAK87821  
ID AAK87821 standard; cDNA; 637 BP.

XX AAK87821;

XX 05-NOV-2001 (first entry)

DE Human digestive system antigen coding sequence SEQ ID NO: 137.

XX Human; digestive system antigen; gene therapy; cancer; appendicitis;  
KM ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;  
KM digestive system disorder; Meckel's diverticulum; ss.

XX Homo sapiens.

XX WO200155314-A2.

PD 02-AUG-2001.

XX 17-JAN-2001; 2001WO-US01324.

XX 31-JAN-2000; 2000US-0179065.

PR 04-FEB-2000; 2000US-0180628.

PR 24-FEB-2000; 2000US-0184664.

PR 02-MAR-2000; 2000US-0186350.

PR 16-MAR-2000; 2000US-0189874.

PR 17-MAR-2000; 2000US-0190076.

PR 18-APR-2000; 2000US-0198123.  
PR 19-MAY-2000; 2000US-0205515.  
PR 07-JUN-2000; 2000US-0209467.  
PR 28-JUN-2000; 2000US-0214886.  
PR 30-JUN-2000; 2000US-0215135.





XX Sequence 637 BP; 142 A; 193 C; 147 G; 150 T; 5 other;

## Query Match

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Best Local Similarity 100.0%; Pred. No. 84;

Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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|||||

Db 362 tgcctcctctgggctctgg 380

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Job time: 3821 sec

GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 19, 2002, 01:16:19 ; Search time 47.29 Seconds  
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5495.459 Million cell updates/sec

Title: US-09-852-845-1

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Post-processing: Listing first 50 summaries

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#### SUMMARIES

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11	18	1.8	7898	4 US-08-984-709A-49	Sequence 49, Appli
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13	18	1.7	410	5 PCT-US96-08623-1	Sequence 1, Appli
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27	18	1.7	11748	1 US-08-611-107-30	Sequence 30, Appli

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29	17	1.6	507	4 US-08-894-818B-26	Sequence 26, Appli
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50	17	1.6	1962	4 US-09-445-472-15	Sequence 15, Appli

RESULT 1  
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; Sequence 1, Application US/08147784  
; Patent No. 5821332  
; GENERAL INFORMATION:  
; APPLICANT: Godfrey, Wayne  
; APPLICANT: Buck, David  
; APPLICANT: Engleman, Edgar G.  
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
; NUMBER OF SEQUENCES: 2  
; CD4+ T-CELLS: ACT-4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,784  
; FILING DATE: 03-NOV-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 05490A-220  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2420  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1057 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; HYPOTHETICAL: NO  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 15..845





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Qy	481	AGCGCGGCGCAGCAATAGCTCTGAGCGCAATCTGTGAGAGCAGGGAGACCCCAAGCACAGC	540
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: Patent No. 5759546			
: GENERAL INFORMATION:			
: APPLICANT: Andrew D. Weinberg and Arthur A.			
: APPLICANT: Vandenberg			
: TITLE OF INVENTION: TREATMENT OF CD4 T-CELL			
: TITLE OF INVENTION: MEDIATED CONDITIONS			
: NUMBER OF SEQUENCES: 3			
: CORRESPONDENCE ADDRESS:			
: ADDRESSEE: Richard J. Polley, Esq.			
: ADDRESSEE: Klarquist Sparkman Campbell			
: ADDRESSEE: Leigh & Whinston			
: STREET: 121 S.W. Salmon Street, Suite 1600			
: CITY: Portland			
: STATE: Oregon			
: COUNTRY: United States of America			
: ZIP: 97204			
: COMPUTER READABLE FORM:			
: MEDIUM TYPE: Disk, 3-1/2 inch			
: COMPUTER: IBM PC compatible			
: OPERATING SYSTEM: MS DOS			
: SOFTWARE: WordPerfect 5.1			
: CURRENT APPLICATION DATA:			
: APPLICATION NUMBER: US/08/192,480A			
: FILING DATE:			
: CLASSIFICATION: 424			
: PRIOR APPLICATION DATA: N/A			
: APPLICATION NUMBER:			

```

1      FILING DATE:
2      ATTORNEY/AGENT INFORMATION:
3      NAME: Richard J. Polley, Esq.
4      REGISTRATION NUMBER: 28,107
5      REFERENCE/DOCKET NUMBER: 4282-38649
6      TELECOMMUNICATION INFORMATION:
7      TELEPHONE: (503) 226-7391
8      TELEFAX: (503) 228-9446
9      INFORMATION FOR SEQ ID NO: 1:
10     SEQUENCE CHARACTERISTICS:
11     LENGTH: 848 base pairs
12     TYPE: Nucleic acid
13     STRANDEDNESS: Double
14     TOPOLOGY: Linear
15     MOLECULE TYPE: cDNA to mRNA
16     HYPOTHETICAL: NO
17     ANTI-SENSE: NO
18     FRAGMENT TYPE:
19     US-08-192-480A-1
20
21     Query Match      27.7%; Score 293; DB 1; Length 848;
22     Best Local Similarity 100.0%; Pred. No. 1e-120;
23     Matches 293; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
24
25     QY      3      gcaagagacgagatgtggtgtggggtctcgcgcgcttgggcccgggacggtgtgcggtctg 62
26             |||||
27     DB      3      GCAGAGACGAGATGTGGTGGGGCTCGGGCGCTGGGCCCGCGGGCCGTGTGGGCTGTG 62
28
29     QY      63      ctctctcttgggcttggggtctgagcaacctgacgggtctcaactgtgtcgggaaacctac 122
30             |||||
31     DB      63      CTCCTCTGGGGCTTGGGCTTGAGCACCGTGAGAGGGGGCTCTCACTGTGTGGGACACCTAC 122
32
33     QY      123     cccaagcaacgacggtgtgtgtccagagtgcaagccagggacagggatgtgtgacggtcgc 182
34             |||||
35     DB      123     CCCACACAGACGCGGTGCTGCCACGAGTGTGACAGCCAGCAGCGAGTGTGACCGCTGC 182
36
37     QY      183     agcgcgtcccaagacaacaggtgtgtccgtccgtcgtgtggggtcgcggtctctacaagacgtgtgc 242
38             |||||
39     DB      183     AGCCCCCTCCCAACACAGGTGTGCGGTCCGTCCGGGGCGCGGCTTTCACACACGCTGGTC 242
40
41     QY      243     agctcgaagcgtgtgcaagccctctcacgtgtgttgaacctcagaagtgaggatga 295
42             |||||
43     DB      243     AGCTCAAGCCGTGCAAGCCCTGCACAGCTGTGTATACCTCAGAAAGTGGAGTGA 295
44
45 RESULT 5
46 US-08-097-827-6
47 : Sequence 6, Application US/08097827
48 : GENERAL INFORMATION:
49 : APPLICANT: Baum, Peter
50 :               Goodman, Ray
51 :               Fanslow, William
52 :               Gayle, Richard
53 : TITLE OF INVENTION: Novel Cytokine Which is a Ligand for
54 :                   OX40
55 : NUMBER OF SEQUENCES: 13
56 : CORRESPONDENCE ADDRESSES:
57 :   ADDRESSEE: Immunex Corporation
58 :   STREET: 51 University Street
59 :   CITY: Seattle
60 :   STATE: WA
61 :   COUNTRY: USA
62 :   ZIP: 98101
63 : COMPUTER READABLE FORM:
64 :   MEDIUM TYPE: floppy disk
65 :   COMPUTER: IBM PC compatible
66 :   OPERATING SYSTEM: PC-DOS/MS-DOS
67 :   SOFTWARE: PatentIn Release #1.0, Version #1.25
68 : CURRENT APPLICATION DATA:
69 :   APPLICATION NUMBER: US/08/097,827
70 :   FILING DATE: 23-Jul-1993
71 :   CLASSIFICATION: <Unknown>
72 :

```

ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOUSE OX40  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..618  
SEQUENCE DESCRIPTION: SEQ ID NO: 6:  
US-08-097-827-6

Query Match 2.6%; Score 28; DB 1; Length 618;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 aaaccaggcctgcaagccctgaccaa 451  
Db 404 ACAACGAGCCTGCAAGCCTGACCAA 431

RESULT 6  
US-08-494-574-6  
Sequence 6, Application US/08494574  
Patent No. 5783665  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for  
TITLE OF INVENTION: OX40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,574  
FILING DATE: 22-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 618 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA to mRNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOUSE OX40  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..618  
US-08-494-574-6

Query Match 2.6%; Score 28; DB 1; Length 618;  
Best Local Similarity 100.0%; Pred. No. 0.0015;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 424 aaaccaggcctgcaagccctgaccaa 451  
Db 404 ACAACGAGCCTGCAAGCCTGACCAA 431

RESULT 7  
US-08-097-827-10  
Sequence 10, Application US/08097827  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: Novel Cytokine which is a ligand for  
TITLE OF INVENTION: OX40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-JUL-1993  
CLASSIFICATION: <Unknown>  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1317 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOX40fc Mutein  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1317  
SEQUENCE DESCRIPTION: SEQ ID NO: 10:  
US-08-097-827-10

Query Match 2.6%; Score 28; DB 1; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 acaccagcctgcaagcctggaccac 451  
|||||  
DB 404 ACACACGCGCTGCACGCCCTGGACCAA 431

## RESULT 8

US-08-494-574-10  
; Sequence 10, Application US/08494574  
; Patent No. 5783665

## GENERAL INFORMATION:

APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for  
TITLE OF INVENTION: OX40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA

ZIP: 98101

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,574  
FILING DATE: 22-JUN-1995  
CLASSIFICATION: 530

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1317 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
IMMEDIATE SOURCE:  
CLONE: MOX40Fc Mutein

FEATURE:  
NAME/KEY: CDS  
LOCATION: 1..1317  
US-08-494-574-10

Query Match 2.6%; Score 28; DB 1; Length 1317;  
Best Local Similarity 100.0%; Pred. No. 0.0014;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 424 acaccagcctgcaagcctggaccac 451  
|||||  
DB 404 ACACACGCGCTGCACGCCCTGGACCAA 431

## RESULT 9

US-08-192-480A-2  
; Sequence 2, Application US/08192480A  
; Patent No. 5759546

## GENERAL INFORMATION:

APPLICANT: Andrew D. Weinberg and Arthur A.  
APPLICANT: Vandenberg  
TITLE OF INVENTION: TREATMENT OF CD4 T-CELL  
TITLE OF INVENTION: MEDIATED CONDITIONS  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Richard J. Polley, Esq.  
ADDRESSEE: Klarquist Sparkman Campbell  
ADDRESSEE: Leigh & Whinston  
STREET: 121 S.W. Salmon Street, Suite 1600  
CITY: Portland  
STATE: Oregon  
COUNTRY: United States of America

ZIP: 97204

## COMPUTER READABLE FORM:

MEDIUM TYPE: Disk, 3-1/2 inch  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: MS DOS  
SOFTWARE: Wordperfect 5.1

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/192,480A  
FILING DATE:  
CLASSIFICATION: 424

PRIOR APPLICATION DATA: N/A  
APPLICATION NUMBER:  
FILING DATE:

ATTORNEY/AGENT INFORMATION:  
NAME: Richard J. Polley, Esq.  
REGISTRATION NUMBER: 28,107  
REFERENCE/DOCKET NUMBER: 4282-38649

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (503) 226-7391  
TELEFAX: (503) 228-9446  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 24 base pairs  
TYPE: Nucleic acid  
STRANDEDNESS: Single  
TOPOLOGY: linear

HYPOTHETICAL: NO  
ANTI-SENSE: NO  
US-08-192-480A-2

Query Match 2.3%; Score 24; DB 1; Length 24;  
Best Local Similarity 100.0%; Pred. No. 0.11;  
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 atgtcgctggggcctgcgcgcgtg 38  
|||||  
DB 1 ATGTGCGTGGGCGCTGCGCGCGCTG 24

## RESULT 10

US-08-984-709A-52/C  
; Sequence 52, Application US/08984709A  
; Patent No. 6320032

## GENERAL INFORMATION:

APPLICANT: Williams, Mark E.  
APPLICANT: Stauderman, Kenneth A.  
APPLICANT: Harpold, Michael M.  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, Suite 700  
CITY: La Jolla



STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,709A  
FILING DATE: 02-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 587-5360  
INFORMATION FOR SEQ ID NO: 52:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1413 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
US-08-984-709A-52

Query Match 1.8%; Score 19; DB 4; Length 1413;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 cctggcctgggacctgctg 686  
|||||  
Db 1313 cctggcctgggacctgctg 1295

RESULT 11  
US-08-984-709A-49/C  
Sequence 49, Application US/08984709A  
Patent No. 6320032  
GENERAL INFORMATION:  
APPLICANT: Williams, Mark E.  
APPLICANT: Stauderman, Kenneth A.  
APPLICANT: Harpold, Michael M.  
TITLE OF INVENTION: HUMAN CALCIUM CHANNEL COMPOSITIONS AND  
TITLE OF INVENTION: METHODS  
NUMBER OF SEQUENCES: 52  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Heller Ehrman White & McCauliffe  
STREET: 4250 Executive Square, Suite 700  
CITY: La Jolla  
STATE: California  
COUNTRY: US  
ZIP: 92037  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/984,709A  
FILING DATE: 02-DEC-1997  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Seidman, Stephanie L.  
REGISTRATION NUMBER: 33,779  
REFERENCE/DOCKET NUMBER: 24735-9815 (formerly 6362-9815)

TELECOMMUNICATION INFORMATION:  
TELEPHONE: (619) 450-8400  
TELEFAX: (619) 587-5360  
INFORMATION FOR SEQ ID NO: 49:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7898 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
FRAGMENT TYPE:  
ORIGINAL SOURCE:  
FEATURE:  
NAME/KEY: Coding Sequence  
LOCATION: 249...7307  
OTHER INFORMATION:  
US-08-984-709A-49

Query Match 1.8%; Score 19; DB 4; Length 7898;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 668 cctggcctgggacctgctg 686  
|||||  
Db 2518 cctggcctgggacctgctg 2500

RESULT 12  
US-09-114-146-1  
Sequence 1, Application US/09114146  
Patent No. 6083747  
GENERAL INFORMATION:  
APPLICANT: Wong, Peter M.C.  
APPLICANT: HAN, Xiaodong  
TITLE OF INVENTION: GLYCOPROTEIN GPI05 ON BLS HEMATOPOIETIC  
TITLE OF INVENTION: STEM CELLS  
NUMBER OF SEQUENCES: 1  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/114,146  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/471,188  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Bent, Stephen A.  
REGISTRATION NUMBER: 29,768  
REFERENCE/DOCKET NUMBER: 46074/102/FEIN  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202)672-5300  
TELEFAX: (202)672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 410 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single

;; TOPOLOGY: linear  
US-09-114-146-1

Query Match 1.7%; Score 18; DB 3; Length 410;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 685 tgcctgggagctgctggcc 702  
|||||  
DB 247 TCGTGGGCTGCTGGGCC 264

RESULT 13  
PCT-US96-08623-1  
; Sequence 1, Application PC/TUS9608623  
; GENERAL INFORMATION:  
; APPLICANT:  
; TITLE OF INVENTION: GLYCOPROTEIN GP105 ON BLS HEMATOPOIETIC  
; TITLE OF INVENTION: STEM CELLS  
; NUMBER OF SEQUENCES: 1  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Foley & Lardner  
; STREET: 3000 K Street, N.W., Suite 500  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20007-5109  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: PCT/US96/08623  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/471,188  
; FILING DATE: 06-JUN-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Bent, Stephen A.  
; REGISTRATION NUMBER: 29,768  
; REFERENCE/DOCKET NUMBER: 46074/103/FEIN  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (202)672-5300  
; TELEFAX: (202)672-5399  
; TEX: 904136  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 410 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
PCT-US96-08623-1

Query Match 1.7%; Score 18; DB 5; Length 410;  
Best Local Similarity 100.0%; Pred. No. 40;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 685 tgcctgggagctgctggcc 702  
|||||  
DB 247 TCGTGGGCTGCTGGGCC 264

RESULT 14  
US-08-934-386-1/c  
; Sequence 1, Application US/08934386  
; Patent No. 6306636  
; GENERAL INFORMATION:  
; APPLICANT: Haselkorn, Robert  
; APPLICANT: Gornicki, Piotr  
; TITLE OF INVENTION: Methods for Detecting Nucleic Acid

;; TITLE OF INVENTION: Segments Encoding Acetyl-CoA Carboxylase  
; NUMBER OF SEQUENCES: 68  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: US  
; ZIP: 77210-4433  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentln Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/934,386  
; FILING DATE: 19-SEP-1997  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Kitchell, Barbara S.  
; REGISTRATION NUMBER: 33,928  
; REFERENCE/DOCKET NUMBER: ARSB:521  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (512) 418-3000  
; TELEFAX: (713) 789-2679  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 1645 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-934-386-1

Query Match 1.7%; Score 18; DB 4; Length 1645;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 681 ctggctgggagctgctg 698  
|||||  
DB 699 CTGGCTGGGCTGCTGCTG 682

RESULT 15  
US-08-893-852A-2/c  
; Sequence 2, Application US/08893852A  
; Patent No. 6080558  
; GENERAL INFORMATION:  
; APPLICANT: Bandman, Olga  
; APPLICANT: Lal, Preeti  
; APPLICANT: Shah, Purvi  
; APPLICANT: Corley, Neil C.  
; TITLE OF INVENTION: NEW HUMAN GROWTH REGULATOR PROTEIN  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Incyte Pharmaceuticals, Inc.  
; STREET: 3174 Porter Drive  
; CITY: Palo Alto  
; STATE: CA  
; COUNTRY: USA  
; ZIP: 94304  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/893,852A  
; FILING DATE: Filed Herewith  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:

NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0341 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2344 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: TML3DT01  
CLONE: 508302  
US-08-893-852A-2

Query Match 1.7%; Score 18; DB 3; Length 2344;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 62 gctcctcctgggctggtg 79  
|||||

Db 2032 GCTCCTCGGCGCTGGG 2015

RESULT 16  
US-08-279-270A-2  
Sequence 2, Application US/08279270A  
Patent No. 5691460  
GENERAL INFORMATION:  
APPLICANT: Duvic, Madeleine  
TITLE OF INVENTION: Epidermal Surface Antigen and Uses  
NUMBER OF SEQUENCES: 3  
CURRENT APPLICATION DATA:  
ADDRESS: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/279, 270A  
FILING DATE: Concurrently herewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Mayfield, Denise L.  
REGISTRATION NUMBER: 33,732  
REFERENCE/DOCKET NUMBER: UTS#173--1/MAY  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/320-7200  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2488 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-279-270A-2

Query Match 1.7%; Score 18; DB 1; Length 2488;  
Best Local Similarity 100.0%; Pred. No. 35;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 669 ctgggcttgggctgtg 686  
|||||

Db 72 CTGGGCTGGGCTGTG 89

RESULT 17  
US-08-188-228-53/c  
Sequence 53, Application US/08188228  
Patent No. 5597725  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shintaro  
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/188,228  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/049,460  
FILING DATE: 19 APR 1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/872,643  
FILING DATE: 17 APR 1992  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5597725and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2550 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
US-08-188-228-53

Query Match 1.7%; Score 18; DB 1; Length 2550;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 663 gccatcctgggctgggc 680  
|||||

Db 990 GCCATCCTGGGCTGGGC 973

RESULT 18  
US-08-332-643-47/c  
Sequence 47, Application US/08332643  
Patent No. 5639634  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shintaro  
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
NUMBER OF SEQUENCES: 56  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
ADDRESSEE: Bicknell  
STREET: Two First National Plaza, 20 South Clark  
STREET: Street  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60603  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332,643  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/07/872,643  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5639634and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 27866/30795  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 346-5750  
TELEFAX: (312) 984-9740  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 47:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2550 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-332-643-47

Query Match 1.7%; Score 18; DB 1; Length 2550;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 gccatcctggcctgggc 680  
|||||  
DB 990 gccatcctggcctgggc 973

RESULT 19  
US-08-332-638-53/C  
Sequence 53, Application US/08332638  
Patent No. 5646250  
GENERAL INFORMATION:  
APPLICANT: Suzuki, Shintaro  
TITLE OF INVENTION: CADHERIN MATERIALS AND METHODS  
NUMBER OF SEQUENCES: 62  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &  
STREET: 6300 Sears Tower, 233 S. Wacker Drive  
CITY: Chicago  
STATE: Illinois  
COUNTRY: USA  
ZIP: 60606  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/332,638  
FILING DATE: 01-NOV-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/872,643  
FILING DATE: 17 APR 1992  
APPLICATION NUMBER: US/08/049,460  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: No. 5646250and, Greta E.  
REGISTRATION NUMBER: 35,302  
REFERENCE/DOCKET NUMBER: 31340  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (312) 474-6300  
TELEFAX: (312) 474-0448  
TELEX: 25-3856  
INFORMATION FOR SEQ ID NO: 53:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2550 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-332-638-53

Query Match 1.7%; Score 18; DB 1; Length 2550;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 663 gccatcctggcctgggc 680  
|||||  
DB 990 gccatcctggcctgggc 973

RESULT 20  
US-08-136-119-3  
Sequence 3, Application US/08136119  
Patent No. 5473056  
GENERAL INFORMATION:  
APPLICANT: Helmbrook, David C.  
APPLICANT: Hoyle, Mona I.  
APPLICANT: Oliff, Allen I.  
TITLE OF INVENTION: E2F-2, A NOVEL MAMMALIAN TRANSCRIPTION  
NUMBER OF SEQUENCES: 29  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: David A. Muthard  
STREET: P.O. Box 2000, 126 Lincoln Avenue  
CITY: Rahway  
STATE: N.J.  
COUNTRY: USA  
ZIP: 07065-0907  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/136,119  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Muthard, David A.  
REGISTRATION NUMBER: 35,297  
REFERENCE/DOCKET NUMBER: 19042  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (908)594-3903  
TELEFAX: (908)594-4720  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 2647 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: CDNA  
US-08-136-119-3

Query Match 1.7%; Score 18; DB 1; Length 2647;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 566 cagcccatcactgtcca 583  
|||||  
Db 2200 CAGGCCATCACTGTCCA 2217

RESULT 21  
US-08-781-802-7  
; Sequence 7, Application US/08781802  
; Patent No. 5969121  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Larry  
; APPLICANT: AIKENS, John  
; APPLICANT: FONSTEIN, Michael  
; APPLICANT: VONSTEIN, Veronika  
; APPLICANT: DEMIRJIAN, David  
; APPLICANT: CASADABAN, Malcolm  
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
; NUMBER OF SEQUENCES: 12  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff  
; STREET: 300 S. Wacker Drive 32nd Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/781,802  
; FILING DATE: 10-JAN-1997  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/694,078  
; FILING DATE: 07-AUG-1996  
; CLASSIFICATION: 536  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,580  
; FILING DATE: 12-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/009,704  
; FILING DATE: 11-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,995  
; FILING DATE: 01-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chao, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,963-E  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3147 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 245..1231  
; OTHER INFORMATION: /note="Tspa E101 sequence longest  
; OTHER INFORMATION: open reading frame; other possible start codons are TTG/Leu9;  
; OTHER INFORMATION: TTG/Leu13; TTG/Leu15; GTG/Val43"

FEATURE:  
; NAME/KEY: mat\_peptide  
; LOCATION: 245..1231  
US-08-781-802-7

Query Match 1.7%; Score 18; DB 2; Length 3147;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgctcctcctggcctgg 78  
|||||  
Db 2214 TGCTCCTCCTGGCCTGG 2231

RESULT 22  
US-08-694-078-7  
; Sequence 7, Application US/08694078  
; Patent No. 6218163  
; GENERAL INFORMATION:  
; APPLICANT: ALLEN, Larry  
; APPLICANT: AIKENS, John  
; APPLICANT: FONSTEIN, Michael  
; APPLICANT: VONSTEIN, Veronika  
; APPLICANT: DEMIRJIAN, David  
; APPLICANT: CASADABAN, Malcolm  
; TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff, Ltd.  
; STREET: 300 S. Wacker Drive 7th Floor  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: USA  
; ZIP: 60606  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/694,078  
; FILING DATE: 07-AUG-1996  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/019,580  
; FILING DATE: 12-JUN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/009,704  
; FILING DATE: 10-JAN-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/001,995  
; FILING DATE: 07-AUG-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Chao, Mark  
; REGISTRATION NUMBER: 37,293  
; REFERENCE/DOCKET NUMBER: 95,963-C  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-913-0001  
; TELEFAX: 312-913-0002  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3147 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: CDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 245..1231  
; OTHER INFORMATION: /note="Tspa E101 sequence longest  
; OTHER INFORMATION: open reading frame; other possible start codons are TTG/Le  
; OTHER INFORMATION: TTG/Leu13; TTG/Leu15; GTG/Val43"

FEATURE:  
NAME/KEY: mac\_peptide  
LOCATION: 245..1231  
US-08-694-078-7

Query Match 1.7%; Score 18; DB 4; Length 3147;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgcctcctcctggcctcg 78  
|||||  
Db 2214 tgcctcctcctcctggcctcg 2231

RESULT 23  
US-09-058-260-7  
Sequence 7, Application US/09058260B  
Patent No. 6218167

GENERAL INFORMATION:  
APPLICANT: Allen, Larry  
APPLICANT: Alkens, John  
APPLICANT: Fousteln, Michael  
APPLICANT: Vonstele, Veronika  
APPLICANT: Demirjian, David  
APPLICANT: Casadaban, Malcolm  
TITLE OF INVENTION: Stable Biocatalysts for Ester Hydrolysis  
FILE REFERENCE: 95-963-H  
CURRENT APPLICATION NUMBER: US/09/058,260B  
EARLIER FILING DATE: 1999-04-10  
EARLIER APPLICATION NUMBER: 60/001,995  
EARLIER FILING DATE: 1996-08-07  
EARLIER APPLICATION NUMBER: 60/009,704  
EARLIER FILING DATE: 1996-01-11  
EARLIER APPLICATION NUMBER: 60/019,580  
EARLIER FILING DATE: 1996-06-12  
EARLIER APPLICATION NUMBER: 08/694,078  
EARLIER FILING DATE: 1996-08-08  
EARLIER APPLICATION NUMBER: 08/781,802  
EARLIER FILING DATE: 1997-01-10  
EARLIER APPLICATION NUMBER: 08/827,810  
EARLIER FILING DATE: 1997-04-11  
NUMBER OF SEQ ID NOS: 37  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 7  
LENGTH: 3147  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: cloned esterase  
OTHER INFORMATION: gene from bacteria E101  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (245)..(1231)  
US-09-058-260-7

Query Match 1.7%; Score 18; DB 4; Length 3147;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 61 tgcctcctcctggcctcg 78  
|||||  
Db 2214 tgcctcctcctcctggcctcg 2231

RESULT 24  
US-08-611-107-32/C  
Sequence 32, Application US/08611107  
Patent No. 5801233  
GENERAL INFORMATION:  
APPLICANT: Haselkorn, Robert  
APPLICANT: Gornicki, Piotr

TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING  
TITLE OF INVENTION: ACETYL-CoA CARBOXYLASE AND USBS  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
zip: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,107  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 800

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 07/956,700  
FILING DATE: 02-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US93/09340  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 08/422,560  
FILING DATE: 14-APR-1995

ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: ARCD:221  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 32:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 3243 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-611-107-32

Query Match 1.7%; Score 18; DB 1; Length 3243;  
Best Local Similarity 100.0%; Pred. No. 34;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 681 ctggtcctcctggcctcctg 698  
|||||  
Db 2300 ctggtcctcctcctggcctcctg 2283

RESULT 25  
US-08-162-146-2/C  
Sequence 2, Application US/08162146  
Patent No. 5965788  
GENERAL INFORMATION:  
APPLICANT: HOUEBINE, Louis-Marie  
APPLICANT: DEVINOY, Eve  
APPLICANT: THEPOT, Dominique  
TITLE OF INVENTION: Production of a Protein of Interest in  
TITLE OF INVENTION: the Milk of a Transgenic Mammalian  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA: US/08/162,146  
APPLICATION NUMBER: US/08/162,146  
FILING DATE: 10-FEB-1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/FR92/00533  
FILING DATE: 12-JUN-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91/07179  
FILING DATE: 12-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4157 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1868..1949, 2462..2587, 2888..3046, 3416  
LOCATION: ..3429)  
US-08-162-146-2

Query Match 1.7%; Score 18; DB 2; Length 4157;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 667 tcctggcctggcctgg 684  
|||||  
Db 901 tcctggcctggcctgg 884

RESULT 26  
US-09-314-127-2/c  
Sequence 2, Application US/09314127  
Patent No. 6268545  
GENERAL INFORMATION:  
APPLICANT: HOUEBINE, Louis-Marie  
APPLICANT: DEVINOV, Eve  
APPLICANT: THEPOT, Dominique  
TITLE OF INVENTION: Production of a Protein of Interest in  
TITLE OF INVENTION: the Milk of a Transgenic Mammalian  
NUMBER OF SEQUENCES: 3  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Foley & Lardner  
STREET: 3000 K Street, N.W., Suite 500  
CITY: Washington  
STATE: D.C.  
COUNTRY: USA  
ZIP: 20007-5109  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/314,127  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/162,146  
FILING DATE:

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: FR 91/07179  
FILING DATE: 12-JUN-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: WEGNER, Harold C.  
REGISTRATION NUMBER: 25,258  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (202) 672-5300  
TELEFAX: (202) 672-5399  
TELEX: 904136  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 4157 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
FEATURE:  
NAME/KEY: CDS  
LOCATION: join(1868..1949, 2462..2587, 2888..3046, 3416  
LOCATION: ..3429)  
US-09-314-127-2

Query Match 1.7%; Score 18; DB 4; Length 4157;  
Best Local Similarity 100.0%; Pred. No. 33;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 667 tcctggcctggcctgg 684  
|||||  
Db 901 tcctggcctggcctgg 884

RESULT 27  
US-08-611-107-30/c  
Sequence 30, Application US/08611107  
Patent No. 5801233  
GENERAL INFORMATION:  
APPLICANT: Haselkorn, Robert  
APPLICANT: Gornickl, Piotr  
TITLE OF INVENTION: NUCLEIC ACID COMPOSITIONS ENCODING  
TITLE OF INVENTION: ACETYL-COA CARBOXYLASE AND USBS  
TITLE OF INVENTION: THEREFOR  
NUMBER OF SEQUENCES: 40  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P. O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: United States of America  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentln Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/611,107  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 800  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 07/956,700  
FILING DATE: 02-OCT-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US PCT/US93/09340  
FILING DATE: 30-SEP-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US SN 08/422,560  
FILING DATE: 14-APR-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Kitchell, Barbara S.  
REGISTRATION NUMBER: 33,928  
REFERENCE/DOCKET NUMBER: ARCD:221  
TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000  
TELEFAX: (512) 474-7577  
INFORMATION FOR SEQ ID NO: 30:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 11748 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-611-107-30

Query Match 1.7%; Score 18; DB 1; Length 11748;  
Best Local Similarity 100.0%; Pred. No. 30;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 681 ctgctgctgggctgctg 698  
|||||  
DB 89 CTGCTGCTGGGCTGCTG 72

## RESULT 28

US-08-905-223-270  
Sequence 270, Application US/08905223  
Patent No. 6222029

GENERAL INFORMATION:  
APPLICANT: Edwards, Jean-Baptiste D.  
APPLICANT: Duclert, Aymeric  
APPLICANT: Lacroix, Bruno  
TITLE OF INVENTION: 5' ESTs FOR SECRETED PROTEINS  
NUMBER OF SEQUENCES: 503  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Knobbe, Martens, Olson & Bear  
STREET: 501 West Broadway  
CITY: San Diego  
STATE: California  
COUNTRY: USA  
ZIP: 92101-3505

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: Win95  
SOFTWARE: Word

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/905,223  
FILING DATE:

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Israelsen, Ned A.  
REGISTRATION NUMBER: 29,655  
REFERENCE/DOCKET NUMBER:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (619) 235-8550  
TELEFAX: (619) 235-0176

INFORMATION FOR SEQ ID NO: 270:  
SEQUENCE CHARACTERISTICS:

LENGTH: 316 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: DOUBLE

TOPOLOGY: LINEAR  
MOLECULE TYPE: CDNA  
ORIGINAL SOURCE:

ORGANISM: Homo Sapiens  
TISSUE TYPE: Brain

FEATURE:

NAME/KEY: other  
LOCATION: 212..311  
IDENTIFICATION METHOD: fasta

OTHER INFORMATION: Identity 93  
OTHER INFORMATION: region 1..101  
OTHER INFORMATION: id HSSCOASN

OTHER INFORMATION: vtl  
FEATURE:

NAME/KEY: other

LOCATION: 243..311  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: Identity 94  
OTHER INFORMATION: region 60..128  
OTHER INFORMATION: id AA135265  
OTHER INFORMATION: est

FEATURE:  
NAME/KEY: other  
LOCATION: 187..245  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: Identity 91  
OTHER INFORMATION: region 3..63  
OTHER INFORMATION: id AA135265  
OTHER INFORMATION: est

FEATURE:  
NAME/KEY: other  
LOCATION: 269..311  
IDENTIFICATION METHOD: blastn  
OTHER INFORMATION: Identity 100  
OTHER INFORMATION: region 49..91  
OTHER INFORMATION: id R58602  
OTHER INFORMATION: est

FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 179..230  
IDENTIFICATION METHOD: Von Heljne matrix  
OTHER INFORMATION: score 4.8  
OTHER INFORMATION: seq ATWVGSSGLAXA/RL

US-08-905-223-270  
Query Match 1.6%; Score 17; DB 4; Length 316;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 635 ggaagtcgccggggggcc 651  
|||||

DB 144 GGAGTCCCGGGGGGCC 160

## RESULT 29

US-08-894-818B-26  
Sequence 26, Application US/08894818B  
Patent No. 6261822

GENERAL INFORMATION:

APPLICANT: TAKAKURA, Hikaru  
APPLICANT: MORISHITA, Mio  
APPLICANT: YAMAMOTO, Katsuhiko

APPLICANT: MITTA, Masanori  
APPLICANT: ASADA, Kiyozo

APPLICANT: TSUNASAWA, Susumu  
APPLICANT: KATO, Ikunoshin

TITLE OF INVENTION: HYPERTHERMOSTABLE PROTEASE GENES  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:

ADDRESSEE: Broadway and Neimark  
STREET: 419 Seventh Street N.W., Ste. 300  
CITY: Washington

STATE: D.C.  
COUNTRY: United States of America  
ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/894,818B  
FILING DATE: 20-MAY-1998  
CLASSIFICATION: 435

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/JP96/03253  
FILING DATE: 07-NOV-1996



PRIOR APPLICATION DATA:  
: APPLICATION NUMBER: JP 323285/1995  
: FILING DATE: 12-DEC-1995  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Browdy, Roger L.  
: REGISTRATION NUMBER: 25,618  
: REFERENCE/DOCKET NUMBER: TAKAKURA-1  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: (202) 628-5197  
: TELEFAX: (202) 737-3528  
: INFORMATION FOR SEQ ID NO: 26:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 507 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: double  
: TOPOLOGY: linear  
: MOLECULE TYPE: genomic DNA  
: US-08-894-818B-26

Query Match 1.6%; Score 17; DB 4; Length 507;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 968 gtctaggtgccgatg 984  
|||||  
Db 383 GTCTAGGTGCCGATGG 399

RESULT 30  
US-08-583-562B-5  
: Sequence 5, Application US/08583562B  
: Patent No. 5922570  
: GENERAL INFORMATION:  
: APPLICANT: Staunton, Donald  
: APPLICANT: Harris, Edith  
: TITLE OF INVENTION: Cytoplasmic Modulators of Integrin  
: TITLE OF INVENTION: Binding  
: NUMBER OF SEQUENCES: 36  
: CORRESPONDENCE ADDRESS:  
: ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
: STREET: 233 South Wacker Drive, 6300 Sears Tower  
: CITY: Chicago  
: STATE: Illinois  
: COUNTRY: USA  
: ZIP: 60606  
: COMPUTER READABLE FORM:  
: MEDIUM TYPE: Floppy disk  
: COMPUTER: IBM PC compatible  
: OPERATING SYSTEM: PC-DOS/MS-DOS  
: SOFTWARE: Patent Release #1.0, Version #1.25  
: CURRENT APPLICATION DATA:  
: APPLICATION NUMBER: US/08/583,562B  
: FILING DATE:  
: CLASSIFICATION: 536  
: ATTORNEY/AGENT INFORMATION:  
: NAME: Williams Jr., Joseph A.  
: REGISTRATION NUMBER: 38,659  
: REFERENCE/DOCKET NUMBER: 27866/33033  
: TELECOMMUNICATION INFORMATION:  
: TELEPHONE: 312-474-6300  
: TELEFAX: 312-474-0448  
: INFORMATION FOR SEQ ID NO: 5:  
: SEQUENCE CHARACTERISTICS:  
: LENGTH: 545 base pairs  
: TYPE: nucleic acid  
: STRANDEDNESS: single  
: TOPOLOGY: linear  
: MOLECULE TYPE: CDNA  
: FEATURE:  
: NAME/KEY: CDS  
: LOCATION: 1..534  
: US-08-583-562B-5

Query Match 1.6%; Score 17; DB 2; Length 545;  
Best Local Similarity 100.0%; Pred. No. 1.1e+02;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 71 gggcctgggctgaagca 87  
|||||  
Db 279 GGGCCTGGGCGCTGAGCA 295

Search completed: June 19, 2002, 02:17:34  
Job time: 3675 sec



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:26:22 ; Search time 17.65 Seconds  
(without alignments)  
1508.031 Million cell updates/sec

Title: US-09-852-845-2  
Perfect score: 277  
Sequence: 1 MCVGARRLGRGPCAALLLLG.....SFRPTIOEQADAHSTLAKI 277

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283138

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database : PIR\_71:\*  
1: pir1:\*  
2: pir2:\*  
3: pir3:\*  
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	277	100.0	277	2 I37552	OX40 homolog - hum
2	271	4.3	271	2 S12783	gene OX40 antigen precu
3	12	4.3	272	2 I48700	hypothetical prote
4	8	2.9	78	2 F28771	hypothetical prote
5	8	2.9	122	2 S56343	hypothetical prote
6	8	2.9	151	2 T43478	hypothetical prote
7	8	2.9	162	2 E70195	colicin V producti
8	8	2.9	215	2 T22446	hypothetical prote
9	8	2.9	236	2 I51740	MHC class II alpha
10	8	2.9	236	2 I51741	MHC class II alpha
11	8	2.9	250	2 JH0749	class II histocomp
12	8	2.9	315	2 H89888	conserved hypotet
13	8	2.9	329	2 S31580	storage protein, b
14	8	2.9	329	2 S17765	major storage prot
15	8	2.9	394	2 C36942	hypothetical prote
16	8	2.9	443	2 D83106	hypothetical prote
17	8	2.9	445	2 B65221	probable amino aci
18	8	2.9	445	2 A91266	probable amino aci
19	8	2.9	445	2 F86106	probable amino aci
20	8	2.9	445	2 AF1022	probable amino aci
21	8	2.9	473	2 G70607	probable amino aci
22	8	2.9	476	2 E87040	acyl-CoA synthase
23	8	2.9	513	2 A95154	sodium/solute sym
24	8	2.9	575	2 D69611	ABC transporter re
25	8	2.9	578	2 A35810	alpha, alpha-trehal
26	8	2.9	583	2 JG6504	alpha, alpha-trehal
27	8	2.9	768	2 T00073	hypothetical prote
28	8	2.9	1031	2 T06130	hypothetical prote
29	7	2.5	52	2 T01742	hypothetical prote

30	7	2.5	88	2 T08512	trbo protein - Ent
31	7	2.5	91	2 B71391	NMDH dehydrogenase
32	7	2.5	93	2 C75603	hypothetical prote
33	7	2.5	96	2 A32954	gro-alpha precursor
34	7	2.5	101	2 B64997	hypothetical prote
35	7	2.5	101	2 B91023	hypothetical prote
36	7	2.5	101	2 C85867	hypothetical prote
37	7	2.5	101	2 AB0506	probable transcrip
38	7	2.5	103	2 D75449	suge protein - Del
39	7	2.5	103	2 AF0795	conserved hypotet
40	7	2.5	116	2 C72232	hypothetical prote
41	7	2.5	119	1 HSD01B	histone H1b, sperm
42	7	2.5	131	2 PQ0059	T-cell receptor be
43	7	2.5	133	2 S76950	hypothetical prote
44	7	2.5	139	2 A81938	probable membrane
45	7	2.5	142	2 AG1555	hypothetical prote
46	7	2.5	142	2 A11197	hypothetical prote
47	7	2.5	149	2 AH0505	probable membrane
48	7	2.5	152	2 A82182	hypothetical prote
49	7	2.5	155	2 F83341	hypothetical prote
50	7	2.5	156	2 AD1175	hypothetical prote

ALIGNMENTS

RESULT 1  
I37552  
OX40 homolog - human  
C:Species: Homo sapiens (man)  
C:Date: 29-May-1998 #sequence\_revision 29-May-1998 #text\_change 11-Jan-2000  
C:Accession: I37552  
R:Latza, U.; Durkop, H.; Schnitger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fo  
Eur. J. Immunol. 24, 677-683, 1994  
A:Title: The human OX40 homolog: cDNA structure, expression and chromosomal assignmen  
A:Reference number: I37552; MUID:94170844  
A:Accession: I37552  
A:Status: preliminary; translated from GR/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <RES>  
A:Cross-references: EMBL:X75962; NID:9472957; PIDN:CA53576.1; PID:9472958  
C:Superfamily: CD27 antigen; NCF receptor repeat homology

Query Match	Best Local Similarity	100.0%	Score 277:	DB 2:	Length 277:
Matches 277:	Conservative	0:	Mismatches	0:	Indels
Gaps	0:				
QY 1	MCVGARRLGRGPCAALLLLGLGLSTVTGLHCYGDYPSNDRCHRCRPGNGVSRCSRSQ	60			
DB 1	MCVGARRLGRGPCAALLLLGLGLSTVTGLHCYGDYPSNDRCHRCRPGNGVSRCSRSQ	60			
QY 61	NTVCRPGCGFYNDVYSSKPKCKTWCNLRSGSERKKQLCTATQDTVCRCRAGTQPLDSYK	120			
DB 61	NTVCRPGCGFYNDVYSSKPKCKTWCNLRSGSERKKQLCTATQDTVCRCRAGTQPLDSYK	120			
QY 121	PGVDCAPCPGPHSGFDNOCAPWNTCTLACGHTLQAPSNSSDAICEDRDPAPATPOETQ	180			
DB 121	PGVDCAPCPGPHSGFDNOCAPWNTCTLACGHTLQAPSNSSDAICEDRDPAPATPOETQ	180			
QY 181	GPPARPITVQPTPEAMPRTSOGSPTRVEYPGGRAVAAILGLGLVGLGPIALILATVLL	240			
DB 181	GPPARPITVQPTPEAMPRTSOGSPTRVEYPGGRAVAAILGLGLVGLGPIALILATVLL	240			
QY 241	RROQLPPDAHKPPGGSFRTPIOEQADAHSTLAKI	277			
DB 241	RROQLPPDAHKPPGGSFRTPIOEQADAHSTLAKI	277			
RESULT 2					
S12783	OX40 antigen precursor - rat				
N:Alternate names:	nerve growth factor receptor homolog				

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C:Species: Rattus norvegicus (Norway rat)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 05-Nov-1999
C:Accession: S12783; S08036
R:Mailet, S.; Fossum, S.; Barclay, A.N.
EMBO J. 9, 1063-1068, 1990
A>Title: Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocyte
A:Reference number: S12783; MUID:90214614
A:Accession: S12783
A:Molecule type: mRNA
A:Residues: 1-271 <MAL>
A:Cross-references: EMBL:X17037; NID:957830; PIDN:CAA34897.1; PID:957831
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: growth factor receptor; Transmembrane protein
F:1-19/Domain: signal sequence #status predicted <SIG>
F:20-271/Product: OX40 antigen #status predicted <MAT>
F:211-235/Domain: transmembrane #status predicted <TM>

Query Match 4.3%; Score 12; DB 2; Length 271;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
|||||
DB 135 NOACKPWTNCTL 146

RESULT 3
148700
gene ox40 protein - mouse
N:Alternate names: OX40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 11-Jan-2000
C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Bullmann, J.E.; van den Eertwegh, A.J.; Claassen, E.; Noelle, R.J.;
J. Immunol. 151, 5261-5271, 1993
A>Title: Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell int
A:Reference number: I48700; MUID:94044750
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:q312827; PIDN:CAA79772.1; PID:q312828
R:Bireland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N.
Eur. J. Immunol. 25, 926-930, 1995
A>Title: Gene structure and chromosomal localization of the mouse homologue of rat OX40
A:Reference number: I48334; MUID:95255413
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: OX40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 4.3%; Score 12; DB 2; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.0012;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149
|||||
DB 136 NOACKPWTNCTL 147

RESULT 4
F28771
hypothetical protein C2397 (photosynthetic gene cluster) - Rhodobacter capsulatus
C:Species: Rhodobacter capsulatus
C:Date: 18-Oct-1989 #sequence_revision 18-Oct-1989 #text_change 18-Jun-1993
C:Accession: F28771

```

```

R:Yovan, D.C.; Bylina, E.J.; Alberti, M.; Begusch, H.; Hearst, J.E.
Cell 37, 949-957, 1984
A>Title: Nucleotide and deduced polypeptide sequences of the photosynthetic reaction-
A:Reference number: A90850; MUID:84259352
A:Accession: F28771
A:Molecule type: DNA
A:Residues: 1-78 <YOU>
A:Cross-references: GB:K01183

Query Match 2.9%; Score 8; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 3.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LGLGLVIG 226
|||||
DB 39 LGLGLVIG 46

RESULT 5
S56343
hypothetical protein f122 - Escherichia coli
C:Species: Escherichia coli
C:Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 08-Oct-1999
C:Accession: S56343
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.
Nucleic Acids Res. 23, 2105-2119, 1995
A>Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from
A:Reference number: S56314; MUID:95334362
A:Accession: S56343
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-122 <BUR>
A:Cross-references: EMBL:U14003; NID:q1263172; PIDN:AAA97014.1; PID:9536959
C:Genetics:
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994
A:Start codon: GTG

Query Match 2.9%; Score 8; DB 2; Length 122;
Best Local Similarity 100.0%; Pred. No. 5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAALLLLG 20
|||||
DB 46 CAALLLLG 53

RESULT 6
T43478
hypothetical protein DKFZp434N1535.1 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 21-Jan-2000
R:Poustka, A.; Klein, M.; Mewes, H.W.; Gassenhuber, J.; Wiemann, S.
submitted to the Protein Sequence Database, December 1999
A:Reference number: Z22516
A:Accession: T43478
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-151 <AAA>
A:Cross-references: EMBL:AL133575
A:Experimental source: adult testis; clone DKFZp434N1535
C:Genetics:
A:Note: DKFZp434N1535.1

Query Match 2.9%; Score 8; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 5.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 LGLSTVTG 28
|||||

```

Db 35 LGLSTVWG 42

RESULT 7  
E70195  
collin V production protein homolog - Lyme disease spirochete  
C:Species: Borrelia burgdorferi (Lyme disease spirochete)  
C>Date: 13-Feb-1998 #sequence\_revision 13-Feb-1998 #text\_change 08-Oct-1999  
C:Accession: E70195  
R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lahlhira, R.; White  
son, D.; Peterson, J.; Kerivage, A.R.; Quackenbush, J.; Salzberg, S.; Hanson, M.; Vogt,  
; Bowman, C.; Garland, S.; Fujii, C.; Cotton, M.D.; Horst, K.; Roberts, K.; Hatch, B.  
Nature 390, 580-586, 1997  
A:Authors: Smith, H.O.; Venter, J.C.  
A>Title: Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi.  
A:Reference number: A70100; MUID:98065943  
A:Accession: E70195  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-162 <KLE>  
A:Cross-references: GB:AE001176; GB:AE000783; NID:g2688699; PIDN:AC67114.1; PID:g268870  
A:Experimental source: strain B31

Query Match 2.9%; Score 8; DB 2; Length 162;  
Best Local Similarity 100.0%; Pred. No. 6.2;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 221 LGLVLGL 228  
|||||||  
Db 107 LGLVLGL 114

RESULT 8  
T22446  
hypothetical protein F49E12.7 - Caenorhabditis elegans  
C:Species: Caenorhabditis elegans  
C>Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T22446  
R:Thomas, K.  
Submitted to the EMBL Data Library, October 1995  
A:Reference number: Z19565  
A:Accession: T22446  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-215 <MTL>  
A:Cross-references: EMBL:Z66520; PIDN:CAA91386.1; GSPDB:GND0020; CESP:F49E12.7  
A:Experimental source: clone F49E12  
C:Genetics:  
A:Gene: CESP:F49E12.7  
A:Map position: 2  
A:Introns: 44/3; 69/3; 136/1

Query Match 2.9%; Score 8; DB 2; Length 215;  
Best Local Similarity 100.0%; Pred. No. 7.8;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 230 PLAILAL 237  
|||||||  
Db 25 PLAILAL 32

RESULT 9  
I51740  
MHC class II alpha chain - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C>Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Sep-1999  
C:Accession: I51740  
R:Sultmann, H.; Meyer, W.E.; Figueroa, F.; O'Huigin, C.; Klein, J.  
Immunogenetics 38, 408-420, 1993  
A>Title: Zebrafish MHC class II alpha chain-encoding genes: polymorphism, expression, an  
A:Reference number: I51740; MUID:94011091

A:Accession: I51740  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <STL>  
A:Cross-references: GB:L19445; NID:g311192; PID:g311193  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 2.9%; Score 8; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLG 229  
|||||||  
Db 214 GLVLGLG 221

RESULT 10  
I51741  
MHC class II alpha chain - zebra fish  
C:Species: Brachydanio rerio (zebra fish)  
C>Date: 13-Mar-1997 #sequence\_revision 13-Mar-1997 #text\_change 20-Sep-1999  
C:Accession: I51741; I51745  
R:Sultmann, H.; Meyer, W.E.; Figueroa, F.; O'Huigin, C.; Klein, J.  
Immunogenetics 38, 408-420, 1993  
A>Title: zebrafish MHC class II alpha chain-encoding genes: polymorphism, expression,  
A:Reference number: I51740; MUID:94011091  
A:Accession: I51741  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <STL>  
A:Cross-references: GB:L19446; NID:g311194; PID:g311195  
A:Accession: I51745  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-236 <STL>  
A:Cross-references: GB:L19450; NID:g311202; PID:g311203  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology

Query Match 2.9%; Score 8; DB 2; Length 236;  
Best Local Similarity 100.0%; Pred. No. 8.4;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVLGLG 229  
|||||||  
Db 214 GLVLGLG 221

RESULT 11  
JH0749  
class II histocompatibility antigen H-20 alpha chain precursor - mouse  
C:Species: Mus musculus (house mouse)  
C>Date: 10-Jun-1993 #sequence\_revision 10-Jun-1993 #text\_change 21-Jan-2000  
C:Accession: JH0749  
R:Karlsson, L.; Peterson, P.A.  
J Exp Med 176, 477-483, 1992  
A>Title: The alpha chain gene of H-20 has an unexpected location in the major histoco  
A:Reference number: JH0749; MUID:92364550  
A:Accession: JH0749  
A:Molecule type: mRNA  
A:Residues: 1-250 <KAR>  
A:Cross-references: GB:M95514; NID:g199312; PIDN:AAB46387.1; PID:g199313  
A:Experimental source: splenocyte  
C:Genetics:  
A:Introns: 28/1; 111/1; 205/1; 250/2  
C:Superfamily: class II histocompatibility antigen; immunoglobulin homology  
C:Keywords: glycoprotein; heterodimer; transmembrane protein  
F:1-25/Domain: signal sequence #status predicted <SIG>  
F:26-250/Product: class II histocompatibility antigen H-20 alpha chain #status predic  
F:126-191/Domain: immunoglobulin homology <IMM>  
F:219-240/Domain: transmembrane #status predicted <TM>  
F:104,144/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Query Match          2.9%; Score 8; DB 2; Length 250;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 220 GGLVGL 227
DB 222 GGLVGL 229

RESULT 12
H89888
Conserved hypothetical protein SA1016 [Imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001
C:Accession: H89888
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.;
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89888
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-315 <KUR>
A:Cross-references: GB:BA000018; PID:g13700972; PIDN:BAB42268.1; GSPDB:GN00149
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1016

Query Match          2.9%; Score 8; DB 2; Length 315;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GVLGLG 229
DB 12 GVLGLG 19

RESULT 13
S31580
Storage protein, bark - cottonwood
C:Species: Populus deltoides (cottonwood)
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Sep-1997
C:Accession: S31580
R:Coleman, G.D.; Chen, T.H.H.
Submitted to the EMBL Data Library, December 1992
A:Reference number: S31580
A:Accession: S31580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-329 <COL>
A:Cross-references: EMBL:X70064; NID:g20464; PID:g20465
C:Genetics:
A:Introns: 102/1; 153/1; 216/1; 274/2

Query Match          2.9%; Score 8; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 7 AALLLGL 14

RESULT 14
S17765
Major storage protein - Carolina poplar
C:Species: Populus x canadensis (Carolina poplar)

```

```

C:Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Sep-1997
C:Accession: S17765; S25320
R:Clausen, S.; Apel, K.
Plant Mol. Biol. 17, 669-678, 1991
A:Title: Seasonal changes in the concentration of the major storage protein and its m
A:Reference number: S17765; MUID:92003681
A:Accession: S17765
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-329 <CLA>
A:Cross-references: GB:S59422; NID:9237632; PID:9237633
A:Note: the authors translated the codon CNG for residues 15 and 16 as Leu, TTT for r
R:Clausen, S.; Apel, K.
Plant Mol. Biol. 20, 365, 1992
A:Title: Seasonal changes in the concentration of the major storage protein and its m
A:Reference number: S25320; MUID:93004495
A:Accession: S25320
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 15-19 <CL2>

Query Match          2.9%; Score 8; DB 2; Length 329;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 7 AALLLGL 14

RESULT 15
C36942
Hypothetical protein PA4219 [Imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 07-Jul-1995 #sequence_revision 07-Jul-1995 #text_change 06-Oct-2000
C:Accession: C36942; G83119
R:Ankenbauer, R.G.; Quan, H.N.
J. Bacteriol. 176, 307-319, 1994
A:Title: FpA, the Fe(III)-pyochelin receptor of Pseudomonas aeruginosa: a phenolate
A:Reference number: A36942; MUID:94117363
A:Accession: C36942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <ANK>
A:Cross-references: GB:U03161; NID:9454352; PIDN:AAQ3215.1; PID:9454355
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.;
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; L
.. Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pa
A:Reference number: A82950; MUID:20437337
A:Accession: G83119
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-394 <STO>
A:Cross-references: GB:AE004638; GB:AE004091; NID:9950422; PIDN:AAQ7607.1; GSPDB:GN
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA4219
C:Superfamily: Pseudomonas aeruginosa hypothetical protein (fpA 3' region)

Query Match          2.9%; Score 8; DB 2; Length 394;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 280 AALLLGL 287

```

RESULT 16  
D83106  
hypothetical protein PA4323 [imported] - Pseudomonas aeruginosa (strain PA01)  
C:Species: Pseudomonas aeruginosa  
C:Date: 15-Sep-2000 #sequence\_revision 15-Sep-2000 #text\_change 31-Dec-2000  
C:Accession: D83106  
R:Stover, C.K.; Plam, X.O.; Eryln, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Br  
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Lardig, K.; Lim,  
; Lory, S.; Olson, M.V.  
Nature 406, 959-964, 2000  
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho  
A:Reference number: A82950; MUID:20437337  
A:Accession: D83106  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-443 <STO>  
A:Cross-references: GB:AE004848; GB:AE004091; NID:g9950537; PIDN:AG07711.1; GSPDB:GN001  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA4323

Query Match 2.9%; Score 8; DB 2; Length 443;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 14 CAALLLGL 21  
| | | | | | | |  
DB 44 AALLLGL 51

RESULT 17  
B65221  
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain K-12  
N:Alternate names: hypothetical protein f326a  
C:Species: Escherichia coli  
C:Date: 12-Sep-1997 #sequence\_revision 17-Sep-1997 #text\_change 02-Nov-2001  
C:Accession: B65221; S56344  
R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; CC  
Science 277, 1453-1462, 1997  
A:Title: The complete genome sequence of Escherichia coli K-12.  
A:Reference number: A64720; MUID:97426617  
A:Accession: B65221  
A:Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-445 <BLAT>  
A:Cross-references: GB:AE000484; GB:U00096; NID:g2367352; PIDN:AAC77076.1; PID:g2367353;  
A:Experimental source: strain K-12, substrain MG1655  
R:Burland, V.; Plunkett III, G.; Sofia, H.J.; Daniels, D.L.; Blattner, F.R.  
Nucleic Acids Res. 23, 2105-2119, 1995  
A:Title: Analysis of the Escherichia coli genome VI: DNA sequence of the region from 92.  
A:Reference number: S56344; MUID:95334362  
A:Accession: S56344  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-321, 'SOMR', 326 <BUR>  
A:Cross-references: EMBL:U14003; NID:g1263172; PIDN:AA97015.1; PID:g536960  
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1994  
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 13 CAALLLGL 20  
| | | | | | | |  
DB 369 CAALLLGL 376

RESULT 18  
A91266

probable amino acid/amine transport protein ECs5097 [imported] - Escherichia coli (st  
C:Species: Escherichia coli  
C:Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 03-Aug-2001  
C:Accession: A91266  
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
gasawara, N.; Yasunaga, T.; Kuhnara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and g  
A:Reference number: A99629; MUID:21156231; PMID:11258796  
A:Accession: A91266  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-445 <HAV>  
A:Cross-references: GB:BA000007; PIDN:BA838520.1; PID:g13364574; GSPDB:GN00154  
A:Experimental source: strain O157:H7, substrain RIMD 0509952  
C:Genetics:  
A:Gene: ECs5097  
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 13 CAALLLGL 20  
| | | | | | | |  
DB 369 CAALLLGL 376

RESULT 19  
F86106  
probable amino acid/amine transport protein [similarity] - Escherichia coli (strain O  
C:Species: Escherichia coli  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 02-Nov-2001  
C:Accession: F86106  
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; May  
iller, L.; Grobeck, E.J.; Davis, N.W.; Lim, A.; Diallanta, E.; Potamouisis, K.; Apoda  
Nature 409, 529-533, 2001  
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A:Reference number: A85480; MUID:21074935; PMID:11206551  
A:Accession: F86106  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-445 <STO>  
A:Cross-references: GB:AF005174; NID:g12519085; PIDN:AG59314.1; GSPDB:GN00145; UMGF:  
A:Experimental source: strain O157:H7, substrain EDL933  
C:Genetics:  
A:Gene: yjde  
C:Superfamily: L-lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 13 CAALLLGL 20  
| | | | | | | |  
DB 369 CAALLLGL 376

RESULT 20  
AF1022  
probable amino acid permease SRY4493 [imported] - Salmonella enterica subsp. enterica  
C:Species: Salmonella enterica subsp. enterica serovar Typhi  
A:Note: This species has also been called Salmonella typhi  
C:Date: 09-Nov-2001 #sequence\_revision 09-Nov-2001 #text\_change 27-Nov-2001  
C:Accession: AF1022  
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Main, J.; Church  
th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farr  
, S.; Moule, S.; O'Garra, P.  
Nature 413, 848-852, 2001  
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens,  
A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica se

A:Reference number: AB0502; PMID:11677608  
A:Accession: AF1022  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-445 <PAR>  
A:Cross-references: GB:AL153382; PIDN:CAM09279.1; PID:g16505283; GSPDB:GN00176  
C:Genetics:  
A:Gene: STY4493  
C:Superfamily: L-Lysine transport protein

Query Match 2.9%; Score 8; DB 2; Length 445;  
Best Local Similarity 100.0%; Pred. No. 14;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAAALLLG 20  
|||||||  
DB 369 CAAALLLG 376

RESULT 21  
G70607  
probable fadD36 protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C>Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 20-Jun-2000  
C:Accession: G70607  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feldwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98293987  
A:Accession: G70607  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-473 <COL>  
A:Cross-references: GB:Z93777; GB:AL123456; NID:93261726; PIDN:CAM07836.1; PID:g1929067  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: fadD36  
C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology  
F:42-469/Domain: acetate--CoA ligase homology <ACCL>

Query Match 2.9%; Score 8; DB 2; Length 473;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVGLLG 229  
|||||||  
DB 184 GLVGLLG 191

RESULT 22  
E87040  
acyl-CoA synthase [imported] - Mycobacterium leprae  
C:Species: Mycobacterium leprae  
C>Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 15-Jun-2001  
C:Accession: E87040  
R:Cole, S.T.; Eiglmeyer, K.; Parkhill, J.; James, K.D.; Thomson, N.R.; Wheeler, P.R.; HC  
R.; Davies, R.M.; Devlin, K.; Dutthoy, S.; Feldwell, T.; Fraser, A.; Hamlin, N.; Holroyd,  
eam, M.A.; Rutherford, K.M.  
Nature 409, 1007-1011, 2001  
A:Authors: Rutter, S.; Seeger, K.; Simon, S.; Simmonds, M.; Skelton, J.; Squares, R.; Sq  
A:Title: Massive gene decay in the leprosy bacillus.  
A:Reference number: A86909; MUID:21128732; PMID:11234002  
A:Accession: E87040  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-476 <STO>  
A:Cross-references: GB:AL450380; NID:g13093059; PIDN:CAC31432.1; GSPDB:GN00147  
C:Genetics:

A:Gene: xclC  
C:Superfamily: 4-coumarate--CoA ligase; acetate--CoA ligase homology

Query Match 2.9%; Score 8; DB 2; Length 476;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVGLLG 229  
|||||||  
DB 187 GLVGLLG 194

RESULT 23  
A95154  
sodium/solute symporter family protein [imported] - Streptococcus pneumoniae (strain  
C:Species: Streptococcus pneumoniae  
C>Date: 03-Aug-2001 #sequence\_revision 03-Aug-2001 #text\_change 03-Aug-2001  
C:Accession: A95154  
R:Retelien, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H  
on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapl  
nson, T.; Hickey, E.K.; Holt, I.E.  
Science 293, 498-506, 2001  
A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morris  
A:Title: Complete genome sequence of a virulent isolate of Streptococcus pneumoniae.  
A:Reference number: A95000; MUID:21357209; PMID:11463916  
A:Accession: A95154  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-513 <KUR>  
A:Cross-references: GB:AE005672; PIDN:AK75426.1; PID:g14972810; GSPDB:GN00164; TIGR:  
A:Experimental source: strain TIGR4  
C:Genetics:  
A:Gene: SPI328

Query Match 2.9%; Score 8; DB 2; Length 513;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVGLLG 229  
|||||||  
DB 414 GLVGLLG 421

RESULT 24  
D69611  
ABC transporter required for expression of cytochrome bd (ATP-) cydD - Bacillus subtil  
C:Species: Bacillus subtilis  
C>Date: 05-Dec-1997 #sequence\_revision 05-Dec-1997 #text\_change 02-Feb-2001  
C:Accession: D69611  
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber  
C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;  
A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,  
Nature 390, 249-256, 1997  
A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal  
iech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M  
koetter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kunita, K.; Lapidus, A.; Lario  
A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Ma  
Y, M.; Oгава, K.; Ogilwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portete  
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanl  
A:Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowata, A.; Se  
kueh, M.; Tanakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiya  
T.; Whitters, P.; Wipac, A.; Yamamoto, H.; Yamane, K.; Yasunoto, K.; Yata, K.; Yoshida  
A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.  
A:Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtil  
A:Reference number: A65580; MUID:98044033  
A:Accession: D69611  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-575 <KUN>  
A:Cross-references: GB:Z99123; GB:AL009126; NID:92636240; PIDN:CAM15899.1; PID:el1863  
A:Experimental source: strain 168



C:Genetics:  
A:Gene: cydD  
C:Superfamily: unassigned ATP-binding cassette proteins; ATP-binding cassette homology  
C:Keywords: ATP; nucleotide binding; P-loop  
F:353-546/Domain: ATP-binding cassette homology <ABC>  
F:370-377/Region: nucleotide-binding motif A (P-loop)

Query Match 2.9%; Score 8; DB 2; Length 575;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 ALLALYL 239  
|||||  
DB 160 ALLALYL 167

RESULT 25  
A35810  
alpha,alpha-trehalase (EC 3.2.1.28) precursor - rabbit  
C:Species: Oryctolagus cuniculus (domestic rabbit)  
C>Date: 23-Oct-1990 #sequence\_revision 23-Oct-1990 #text\_change 02-Jun-2000  
C:Accession: A35810  
R:Rut, J.; Wacker, H.; James, P.; Maffia, M.; Seiler, P.; Galand, G.; von Kieckebusch, A.  
J. Biol. Chem. 265, 15034-15039, 1990  
A:Title: Rabbit small intestinal trehalase. Purification, cDNA cloning, expression, and  
A:Reference number: A35810; MUID:90368681  
A:Accession: A35810  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-578 <RUF>  
A:Cross-references: GB:M55299; NID:g164736; PIDN:AAA63460.1; PID:g164737; GB:M36523  
C:Superfamily: human alpha,alpha-trehalase  
C:Keywords: glycosidase; hydrolase

Query Match 2.9%; Score 8; DB 2; Length 578;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23  
|||||  
DB 11 LLLGLGL 18

RESULT 26  
JC6504  
alpha,alpha-trehalase (EC 3.2.1.28) - human  
C:Species: Homo sapiens (man)  
C>Date: 04-Sep-1998 #sequence\_revision 04-Sep-1998 #text\_change 20-Jun-2000  
C:Accession: JC6504  
R:Ishihara, R.; Taketani, S.; Sasaki-Takedatsu, M.; Kino, M.; Tokunaga, R.; Kobayashi, Y.  
Gene 202, 63-74, 1997  
A:Title: Molecular cloning, sequencing and expression of cDNA encoding human trehalase.  
A:Reference number: JC6504; MUID:98087419  
A:Accession: JC6504  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-583 <ISH>  
A:Cross-references: DDBJ:AB000824; NID:g2789460; PIDN:BA24381.1; PID:g2789461  
C:Superfamily: human alpha,alpha-trehalase  
C:Keywords: glycosidase; hydrolase

Query Match 2.9%; Score 8; DB 2; Length 583;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23  
|||||  
DB 11 LLLGLGL 18

RESULT 27  
T00073  
hypothetical protein KIA0527 - human (fragment)

C:Species: Homo sapiens (man)  
C>Date: 22-Jan-1999 #sequence\_revision 22-Jan-1999 #text\_change 21-Jul-2000  
C:Accession: T00073  
R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara,  
DNA Res. 5, 31-39, 1998  
A:Title: Prediction of the coding sequences of unidentified human genes. IX. The comp  
A:Reference number: Z14086; MUID:98290545  
A:Accession: T00073  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: mRNA  
A:Residues: 1-768 <NAG>  
A:Cross-references: EMBL:AB011099; NID:g3043577; PIDN:BA25453.1; PID:g3043578  
A:Experimental source: brain; clone HG2246  
C:Genetics:  
A:Note: KIA0527

Query Match 2.9%; Score 8; DB 2; Length 768;  
Best Local Similarity 100.0%; Pred. No. 21;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 ALLLLGL 21  
|||||  
DB 161 ALLLLGL 168

RESULT 28  
T06130  
hypothetical protein F23E12.170 - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cress)  
C>Date: 30-Apr-1998 #sequence\_revision 30-Apr-1999 #text\_change 15-Sep-2000  
C:Accession: T06130  
R:Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt, A.; Duesterhoeft, A.; Hoheis  
submitted to the Protein Sequence Database, April 1999  
A:Reference number: Z15485  
A:Accession: T06130  
A:Molecule type: DNA  
A:Residues: 1-1031 <BEV>  
A:Cross-references: EMBL:AL022604; GSPDB:GN00062; ATSP:F23E12.170  
A:Experimental source: cultivar Columbia; BAC clone F23E12  
C:Genetics:  
A:Gene: ATSP:F23E12.170  
A:Map position: 4  
A:Introns: 307/3; 359/2; 682/1; 898/3; 962/1  
C:Superfamily: Arabidopsis thaliana hypothetical protein F23E12.170

Query Match 2.9%; Score 8; DB 2; Length 1031;  
Best Local Similarity 100.0%; Pred. No. 27;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 196 PRTSOGPS 203  
|||||  
DB 143 PRTSOGPS 150

RESULT 29  
T01742  
hypothetical protein 3 - maize mitochondrion  
C:Species: mitochondrion Zea mays (maize)  
C>Date: 19-Feb-1999 #sequence\_revision 19-Feb-1999 #text\_change 29-Oct-1999  
C:Accession: T01742  
R:Smith, A.G.; Ping, D.R.  
Curr. Genet. 12, 617-623, 1987  
A:Title: Nucleotide sequence and molecular characterization of a maize mitochondrial  
A:Reference number: Z14414; MUID:89003167  
A:Accession: T01742  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-52 <SMI>

A:Cross-references: EMBL:M36398; NID:g342649; PIDN:AAA70277.1; PID:g897626  
C:Genetics:  
A:Genome: mitochondrion  
C:Keywords: mitochondrion

Query Match 2.5%; Score 7; DB 2; Length 52;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 6 RRLGRGP 12  
|||||||  
DB 35 RRLGRGP 41

RESULT 30  
T08512

trbO protein - Enterobacter aerogenes plasmid R751

C:Species: Enterobacter aerogenes

C>Date: 11-Jun-1999 #sequence\_revision 11-Jun-1999 #text\_change 21-Jul-2000

C:Accession: T08512

R:Thorsted, P.B.; Shah, D.S.; Macartney, D.; Kostelidou, K.; Thomas, C.M.

Plasmid 36, 95-111, 1996

A>Title: Conservation of the genetic switch between replication and transfer genes of trb

A:Reference number: Z16434; MUID:97118926

A:Accession: T08512

A>Status: Preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-88 <THO>

A:Cross-references: EMBL:U67194; NID:g1572520; PIDN:AAC64456.1; PID:g1572561

C:Genetics:

A:Gene: trbO

A:Genome: plasmid R751

Query Match 2.5%; Score 7; DB 2; Length 88;  
Best Local Similarity 100.0%; Pred. No. 36;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLG 22  
|||||||  
DB 36 LLLGLG 42

Search completed: June 18, 2002, 14:29:51  
Job time: 209 sec

GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:28:52 ; Search time 13.06 Seconds  
(without alignments)  
821.234 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 277

Sequence: 1 MCVGARRLRGPCPALILIG.....SFRPIQEQADAHSTLAKI 277

Scoring table: OLIGO

Searched: 105224 seqs, 38719550 residues

Word size: 0

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 50 summaries

Database: SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	277	100.0	277	1 TNRA_HUMAN	P3489 homo sapien
2	12	4.3	271	1 TNRA_RAT	P15725 ratu
3	12	4.3	272	1 TNRA_MOUSE	P47741 mus musculu
4	9	3.2	625	1 TR11_MOUSE	O35305 mus musculu
5	8	2.9	78	1 PUFK_RHOCA	P26240 rhodobacter
6	8	2.9	394	1 Y6B9_PSEAE	P42514 pseudomonas
7	8	2.9	445	1 YUDE_ECOLI	P39265 escherichia
8	8	2.9	575	1 CYDD_BACSU	P4367 bacillus su
9	8	2.9	578	1 TREB_RABIT	P19813 oryctolagus
10	8	2.9	583	1 TREB_HUMAN	O43280 homo sapien
11	7	2.5	91	1 NULM_BRALA	O79420 brachio
12	7	2.5	96	1 GRO_MOUSE	P12850 mus musculu
13	7	2.5	101	1 ELAB_ECOLI	P52084 escherichia
14	7	2.5	119	1 HIB_PLAUD	P06895 platytreis
15	7	2.5	144	1 CYTF_MOUSE	O89098 mus musculu
16	7	2.5	164	1 P35792_HORVU	P35792 hordeum vul
17	7	2.5	164	1 PRL_HORVU	O05968 hordeum vul
18	7	2.5	173	1 CRAM_MOUSE	P51437 mus musculu
19	7	2.5	173	1 NUGM_ONCRY	P48177 oncorhynch
20	7	2.5	173	1 NUGM_ONCRY	O94222 salmo salar
21	7	2.5	200	1 NUGM_SALSA	P29922 paracoccus
22	7	2.5	260	1 HA2Q_HUMAN	P20036 homo sapien
23	7	2.5	265	1 BXB1_HAEIN	P19390 haemophilus
24	7	2.5	265	1 BXB3_HAEIN	P22235 haemophilus
25	7	2.5	267	1 YG95_HAEIN	O48215 haemophilus
26	7	2.5	269	1 LEPA_SYNT3	P12640 synechocyst
27	7	2.5	283	1 LEPA_ERWCH	P31711 erythrina chr
28	7	2.5	283	1 VBL1_METJA	O38052 methanococc
29	7	2.5	298	1 VBL1_CLVK	P14971 cassava lat
30	7	2.5	298	1 VBL1_CLVK	P14971 cassava lat
31	7	2.5	327	1 DHBL_HUMAN	P14061 homo sapien
32	7	2.5	342	1 ISIA_SYND2	P31157 synechococc
33	7	2.5	354	1 CD68_HUMAN	P34810 homo sapien

34	7	2.5	371	1 Y4OS_RHISN	P55604 rhizobium s
35	7	2.5	373	1 Y4UD_PICAN	P34735 pichia angu
36	7	2.5	377	1 Y4WD_RHISN	P55682 rhizobium s
37	7	2.5	389	1 YS96_MYCRU	O10817 mycobacteri
38	7	2.5	415	1 CRF1_MOUSE	P35347 mus musculu
39	7	2.5	415	1 CRF1_RAT	P35353 ratu
40	7	2.5	415	1 CRF1_SHEEP	O62772 ovys aries
41	7	2.5	428	1 NSD1_PSEAE	O56228 thelurus agu
42	7	2.5	438	1 NMT2_PSEAE	O94P12 pseudomonas
43	7	2.5	441	1 ODBA_RAT	P11960 ratu
44	7	2.5	442	1 ODBA_MOUSE	P50136 mus musculu
45	7	2.5	444	1 CRF1_HUMAN	P34998 homo sapien
46	7	2.5	468	1 YB07_HAEIN	O57007 haemophilus
47	7	2.5	469	1 NCOO_THERH	O56228 thelurus agu
48	7	2.5	498	1 NPS1_SCHPO	O74351 schizosacch
49	7	2.5	548	1 ERF_HUMAN	P50548 homo sapien
50	7	2.5	551	1 ERF_MOUSE	P70459 mus musculu

ALIGNMENTS

RESULT 1

1	TNRA_HUMAN	STANDARD:	PRT:	277 AA.
ID	TNRA_HUMAN			
AC	P43489; O13663;			
DT	01-NOV-1995 (Rel. 32, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (ACT35 antigen) (TAX-transcriptionally activated glycoprotein 1 receptor) (CD134 antigen).			
DE	glycoprotein 1 receptor (CD134 antigen).			
GN	TNFRSF4 OR TNFR4.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=94170844; PubMed=7510240;			
RA	Lutza U., Dueckop H., Schmittiger S., Ringeling J., Eitelbach F., Hummel M., Fonatsch C., Stein H.,			
RA	"The human OX40 homologue: CDNA structure, expression and chromosomal assignment of the ACT35 antigen.";			
RT	Eur. J. Immunol. 24:677-683(1994).			
RL	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=95219871; PubMed=7704935;			
RA	Baum P.R., Gayle R.B. III, Ramsdell F., Srinivasan S., Sorensen R.A., Watson M.L., Seidm M.F., Clifford K.N., Grabstein K., Alderson M.R.;			
RA	"Identification of OX40 ligand and preliminary characterization of its activities on OX40 receptor.";			
RT	Circ. Shock 44:30-34(1994).			
RL	Circ. Shock 44:30-34(1994).			
CC	- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.			
CC	- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.			
CC	- DATABASE: NAME=PROT; NOTE=CD guide CD134 entry;			
CC	WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd134.htm".			
CC	-----			
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CC	-----			
DR	EMBL: X75962; CAA53576.1; -			
DR	HSMR: S76792; AAB33944.1; ALT_INIT.			
DR	HSSP: P25942; ICDF.			
DR	MIM: 600315; -			
DR	InterPro: IPR001368; TNFR_c6.			
DR	Pfam: PF00020; TNFR_c6; 3.			

DR ProDom: PD000771; TNFR\_c6; 1.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR.2; 2.  
 KM Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 Signal.  
 FT SIGNAL 1 28  
 FT CHAIN 29 277  
 FT DOMAIN 29 214  
 FT TRANSMEM 215 235  
 FT DOMAIN 236 277  
 FT REPEAT 30 65  
 FT REPEAT 66 107  
 FT REPEAT 108 126  
 FT REPEAT 127 167  
 FT CAROHD 146 146  
 FT CAROHD 160 160  
 SQ SEQUENCE 277 AA; 29340 MW; 49F15325941550BF CRC64;

Query Match 100.0%; Score 277; DB 1; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 2,66-263; Mismatches 0; Indels 0; Gaps 0;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MCVGARRLGRPCALLLGLSTVGLHVDYPSNDRCHCEPENGWVSRCSRSQ 60  
 DB 1 MCVGARRLGRPCALLLGLSTVGLHVDYPSNDRCHCEPENGWVSRCSRSQ 60  
 QY 61 MIVCPRCGFGFNDVSSPKCKPCMCNLRSGERKOLCTAODYPCRCRAGOPRDSK 120  
 DB 61 MIVCPRCGFGFNDVSSPKCKPCMCNLRSGERKOLCTAODYPCRCRAGOPRDSK 120  
 QY 121 PCVDCAPCPGHFSPDNOACKPWTNCTLAGKHTLOPASNSSDALCEDRPPATOPQETO 180  
 DB 121 PCVDCAPCPGHFSPDNOACKPWTNCTLAGKHTLOPASNSSDALCEDRPPATOPQETO 180  
 QY 181 GPPARITVQPTFEMWRTSGSPSTRVEYPPGGRVAVALIGLGLVGLLPLAILLALYL 240  
 DB 181 GPPARITVQPTFEMWRTSGSPSTRVEYPPGGRVAVALIGLGLVGLLPLAILLALYL 240  
 QY 241 RRDQRLPPDAHKPPGGSFRTPIQEOADAHSTLAKI 277  
 DB 241 RRDQRLPPDAHKPPGGSFRTPIQEOADAHSTLAKI 277

RESULT 2  
 TNFR\_RAT  
 ID TNFR\_RAT STANDARD: PRT: 271 AA.  
 AC P15725:  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen) (MRC OX40).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=T-cell;  
 RA MEDLINE=9021614; PubMed=2157591;  
 RA Mallett S., Fossam S., Barclay A.N.;  
 RT "Characterization of the MRC OX40 antigen of activated CD4 positive T lymphocytes -- a molecule related to nerve growth factor receptor.";  
 RL EMO J 9:1063-1068(1990)  
 CC -1- FUNCTION: RECEPTOR FOR THE OX40L/ GP34 CYTOKINE.  
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.  
 CC -1- TISSUE SPECIFICITY: ACTIVATED T-CELLS.  
 CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.  
 RT -----

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DR EMBL; X17037; CAA34897.1; -  
 DR PIR; S08036; S08036.  
 DR PIR; S12783; S12783.  
 DR HSP; P19438; 1EXT.  
 DR InterPro; IPR001368; TNFR\_c6.  
 DR Pfam; PF00020; TNFR\_c6; 3.  
 DR ProDom; PD000771; TNFR\_c6; 1.  
 DR SMART; SMO0208; TNFR; 3.  
 DR PROSITE; PS00652; TNFR\_NGFR.1; 3.  
 DR PROSITE; PS00500; TNFR\_NGFR.2; 2.  
 KM Receptor; T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;  
 Signal.  
 FT SIGNAL 1 19  
 FT CHAIN 20 271  
 FT DOMAIN 20 210  
 FT TRANSMEM 211 235  
 FT DOMAIN 236 271  
 FT REPEAT 25 60  
 FT REPEAT 61 102  
 FT REPEAT 103 123  
 FT REPEAT 124 164  
 FT CAROHD 143 143  
 SQ SEQUENCE 271 AA; 29895 MW; C06465136B16E821 CRC64;

Query Match 4.3%; Score 12; DB 1; Length 271;  
 Best Local Similarity 100.0%; Pred. No. 0,00042; Mismatches 0; Indels 0; Gaps 0;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
 DB 135 NOACKPWTNCTL 146

RESULT 3  
 TNFR\_MOUSE  
 ID TNFR\_MOUSE STANDARD: PRT: 272 AA.  
 AC P47741:  
 DT 01-FEB-1996 (Rel. 33, Created)  
 DT 01-FEB-1996 (Rel. 33, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Tumor necrosis factor receptor superfamily member 4 precursor (OX40L receptor) (OX40 antigen).  
 GN TNFRSF4 OR TXGPIL OR OX40.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=DALB/C;  
 RX MEDLINE=94044750; PubMed=8228223;  
 RA Calderhead D.M., Buhmann J.E., van den Eertwegh A.J.,  
 RA Claassen E., Noelle R.J., Fell H.;  
 RT "Cloning of mouse OX40: a T cell activation marker that may mediate T-B cell interactions.";  
 RL J. Immunol. 151:5261-5271(1993).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=95255413; PubMed=7737295;  
 RA Birkeland M.L., Copeland N.G., Gilbert D.J., Jenkins N.A.,  
 RA Barclay A.N.;  
 RT "Gene structure and chromosomal localization of the mouse homologue of rat OX40 protein.";  
 RT -----

```

RL Eur. J. Immunol. 25:926-930(1995).
CC -1- FUNCTION: RECEPTOR FOR THE OX40L/GP34 CYTOKINE.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-----
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-----
DR EMBL: Z21674; CAA79727.1; -
DR EMBL: X85214; CAA59476.1; -
DR HSSP: P19438; EXT.
DR MGI: 104512; Tnf1sf4.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRODOM: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 3.
DR PROSITE: PS00652; TNFR_NGFR_1; 3.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
DR Receptor: T-cell; Antigen; Glycoprotein; Transmembrane; Repeat;
KW Signal.
FT SIGNAL 1 19
FT CHAIN 20 272
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 4
FT FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 212 211
FT DOMAIN 212 236
FT FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 26 61
FT REPEAT 62 103
FT REPEAT 104 124
FT REPEAT 125 165
FT CARBOHYD 144 144
FT CONFLICT 15 15
FT SEQUENCE 272 AA; 30153 MW; 06E7B4156FDD08E CRC64;
SQ
Query Match 4.3%; Score 12; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 138 NOACKPWNTCTL 149
DB 136 NOACKPWNTCTL 147
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RESULT 4
TRIL_MOUSE STANDARD; PRT; 625 AA.
ID TRIL_MOUSE
AC 035305;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kB) (osteoclast differentiation factor
DE receptor) (ODFR).
GN TNFRSF11A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=fetal liver;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Gallibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
```

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RL Nature 390:175-179(1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis."
RL Biochem. Biophys. Res. Commun. 253:395-400(1998).
CC -1- FUNCTION: RECEPTOR FOR RANK LIGAND (RANKL; ALSO KNOWN AS
CC OSTEOCLAST DIFFERENTIATION FACTOR OR ODF), ESSENTIAL FOR RANKL-
CC MEDIATED OSTEOCLASTOGENESIS. INVOLVED IN THE REGULATION OF
CC INTERACTIONS BETWEEN T-CELLS AND DENDRITIC CELLS.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UNBIQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC TRABECULAR BONE, THYMUS, SMALL INTESTINE, LUNG, BRAIN AND KIDNEY.
CC WEAKLY EXPRESSED IN SPLEEN AND BONE MARROW.
CC -1- SIMILARITY: CONTAINS 4 TNFR-CYS REPEATS.
-----
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-----
DR EMBL: AF019046; AAB86810.1; -
DR HSSP: P25942; ICDF.
DR MGI: 1314891; Tnf1sf11a.
DR InterPro: IPR001368; TNFR_c6.
DR Pfam: PF00020; TNFR_c6; 3.
DR PRODOM: PD000771; TNFR_c6; 1.
DR SMART: SM00208; TNFR; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; 1.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
DR Receptor: Glycoprotein; Transmembrane; Repeat; Signal.
KW SIGNAL 1 30
FT FT TUMOR NECROSIS FACTOR RECEPTOR
FT FT SUPERFAMILY MEMBER 11A
FT FT EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 215 214
FT DOMAIN 215 234
FT FT CYTOPLASMIC (POTENTIAL).
FT REPEAT 35 625
FT REPEAT 72 113
FT REPEAT 115 152
FT REPEAT 155 195
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 128
FT DISULFID 134 152
FT CARBOHYD 106 106
FT CARBOHYD 175 175
FT SEQUENCE 625 AA; 66621 MW; F8C1872E9511D8E CRC64;
SQ
Query Match 3.2%; Score 9; DB 1; Length 625;
Best Local Similarity 100.0%; Pred. No. 0.75;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 141 CKPWNTCTL 149
DB 170 CKPWNTCTL 178
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RESULT 5
PUFX_RHOCA STANDARD; PRT; 78 AA.
ID PUFX_RHOCA
AC P26240;
DT 01-MAY-1992 (Rel. 22, Created)
```

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DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Intrinsic membrane protein pufX (Protein C2397).
GN pufX.
OS Rhodospirillum rubrum (Rhodospirillum rubrum).
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillum group;
OC Rhodospirillum.
OX NCBI_TaxID=1061;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84259352; PubMed=6744416;
RA Youvan D.C., Bylina E.J., Alberti M., Begusch H., Hearst J.E.;
RT "Nucleotide and deduced polypeptide sequences of the photosynthetic
RT reaction-center, B870 antenna, and flanking polypeptides from R.
RT rubrum."
RL Cell 37:949-957(1984).
CC -1- FUNCTION: ASSOCIATED WITH THE REACTION CENTER - LIGHT-HARVESTING
CC COMPLEX I. MAY PLAY A CRITICAL ROLE IN FACILITATING THE
CC INTERACTION BETWEEN THIS COMPLEX AND OTHER COMPONENTS REQUIRED FOR
CC LIGHT-DRIVEN CYCLIC ELECTRON TRANSFER.
CC -1- SUBCELLULAR LOCATION: INTRACYTOSOLIC MEMBRANE.
CC -1- SIMILARITY: TO PUF FROM R. SPHEROIDES.
CC -----
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CC -----
DR EMBL: Z1165; CAAT7556.1; -
DR EMBL: K01183; -; NOT_ANNOTATED_CDS.
DR PIR: F28771; F28771.
KW Photosynthesis; Membrane.
SQ SEQUENCE 78 AA; 8569 MW; D85FF4097E6D65B0 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 1.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 219 LGGLVGLG 226
DB 39 LGGLVGLG 46

RESULT 6
Y6B9_PSEAE STANDARD; PRT; 394 AA.
AC P42514;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein PA4219.
GN PA4219.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID=287;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=PAO;
RX MEDLINE=9411763; PubMed=8288523;
RA Ankenbauer R.G., Quan H.N.;
RT "Fpva, the Fe(II)-pyochelin receptor of Pseudomonas aeruginosa: a
RT phenolate siderophore receptor homologous to hydroxamate siderophore
RT receptors."
RL J. Bacteriol. 176:307-319(1994).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 15692 / PAOI;
RX MEDLINE=20437337; PubMed=10984043;

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RA Stoyer C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Goltz L., Tolentino E., Westbrock-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Lardig K., Lim R.M.,
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;
RT "Complete genome sequence of Pseudomonas aeruginosa PAOI, an
RT opportunistic pathogen."
RT Nature 406:959-964(2000).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -----
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CC -----
DR EMBL: U03161; AAC43215.1; -
DR EMBL: AE004838; AAG07607.1; -
DR PIR: A00000; A00000.
KW Hypothetical protein; Transmembrane; Complete proteome.
SQ SEQUENCE 394 AA; 42248 MW; 89A0D93871CC71BE CRC64;

Query Match 2.9%; Score 8; DB 1; Length 394;
Best Local Similarity 100.0%; Pred. No. 4.8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLGL 21
DB 280 AALLLGL 287

RESULT 7
YUDE_ECOLI STANDARD; PRT; 445 AA.
AC P39269; P39269;
DT 01-FEB-1995 (Rel. 31, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical transport protein yude.
GN YUDE OR B4115 OR Z5717 OR ECSS097.
OS Escherichia coli.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_TaxID=562, 83334;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=K12 / MG1655;
RX MEDLINE=9534362; PubMed=7610040;
RA Burland V.D., Plunkett G. III, Sofia H.J., Daniels D.L.,
RA Blattner F.R.;
RT "Analysis of the Escherichia coli genome VI: DNA sequence of the
RT region from 92.8 through 100 minutes."
RL Nucleic Acids Res. 23:2105-2119(1995).
RN [2]
RP REVISIONS.
RX STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;

```

RT "The complete genome sequence of Escherichia coli K-12."  
 RL Science 277:1453-1474(1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-0157:H7 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobeck E.J., Davis N.W., Lam A., Dimalanta E.T., Potamoukis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7";  
 RL Nature 409:529-533(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-0157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasakiwa C., Ogasawara N., Yasunaga T.,  
 RA Kihara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 O157:H7 and genomic comparison with a laboratory strain K-12";  
 RL DNA Res. 8:11-22(2001).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
 (potential).  
 CC -1- SIMILARITY: BELONGS TO THE ARCD/CADB/GERAB/LYSI FAMILY OF  
 PERMEASES.  
 CC -----  
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 CC -----  
 DR EMBL: U14003; AAA97015.1; ALT\_FRAME.  
 DR EMBL: U14003; AAA97014.1; ALT\_FRAME.  
 DR EMBL: AE000484; AAC77076.1; -.  
 DR EMBL: AE005644; AAG59314.1; -.  
 DR EMBL: AP002368; BAB38520.1; -.  
 DR EcoGene; EG12462; yjde.  
 DR InterPro: IPR002293; AA\_rel\_permease\_1.  
 DR InterPro: IPR002027; Amino\_acid\_permease.  
 DR Pfam; PF00324; aa\_permeases; 1.  
 KW Hypothetical protein; Transp.; Transmembrane; Inner membrane;  
 KW Complete proteome.  
 FT TRANSMEM 10 30 POTENTIAL.  
 FT TRANSMEM 39 59 POTENTIAL.  
 FT TRANSMEM 99 119 POTENTIAL.  
 FT TRANSMEM 123 143 POTENTIAL.  
 FT TRANSMEM 153 173 POTENTIAL.  
 FT TRANSMEM 197 217 POTENTIAL.  
 FT TRANSMEM 226 246 POTENTIAL.  
 FT TRANSMEM 276 296 POTENTIAL.  
 FT TRANSMEM 322 342 POTENTIAL.  
 FT TRANSMEM 356 376 POTENTIAL.  
 FT TRANSMEM 386 406 POTENTIAL.  
 FT TRANSMEM 409 429 POTENTIAL.  
 SQ SEQUENCE 445 AA; 46842 MW; 359F70C489A20663 CRC64;

Query Match 2.9%; Score 8; DB 1; Length 445;  
 Best Local Similarity 100.0%; Pred. No. 5.3;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 13 CAALLLG 20  
 |||||  
 DB 369 CAALLLG 376

RESULT 8  
 ID CYDD\_BACSU STANDARD; PRT; 575 AA.  
 AC P94367;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE Transport ATP-binding protein cydd.  
 GN CYDD.  
 OS Bacillus subtilis.  
 OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
 OC Bacillus/Staphylococcus group; Bacillus.  
 OC NCBI\_TaxID=1423;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-168 / BGSCL1;  
 RX MEDLINE=97124196; PubMed=8969509;  
 RA Yoshida K.-I., Shindo K., Sano H., Seki S., Fujimura M., Yanai N.,  
 RA Miwa Y., Fujita Y.;  
 RT "Sequencing of a 65 kb region of the Bacillus subtilis genome  
 RT containing the ltc and cel loci, and creation of a 177 kb contig  
 RT covering the gnt-sacxy region";  
 RL Microbiology 142:3113-3123(1996).  
 CC -1- FUNCTION: SOMEHOW INVOLVED IN THE CYTOCHROME D BRANCH OF AEROBIC  
 CC RESPIRATION. SEEMS TO BE A COMPONENT OF A TRANSPORT SYSTEM (BY  
 CC SIMILARITY).  
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).  
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY. MSBA SUBFAMILY.  
 CC -----  
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 CC -----  
 DR EMBL: D83026; BAA11730.1; -.  
 DR EMBL: Z99123; CAB15899.1; -.  
 DR HSSP; P13569; INBD.  
 DR Subtilist; BG11928; cydd.  
 DR InterPro: IPR003593; AAA.  
 DR InterPro: IPR001140; ABC\_transporter\_tmam.  
 DR InterPro: IPR003439; ABC\_transporter.  
 DR InterPro: IPR001687; ATP\_GTP\_A.  
 DR Pfam; PF00664; ABC\_membrane; 1.  
 DR Pfam; PF00005; ABC\_tran; 1.  
 DR SMART; SM00382; AAA; 1.  
 DR PROSITE; PS00211; ABC\_TRANSPORTER; 1.  
 KW ATP-binding; Transport; Transmembrane; Complete proteome.  
 FT TRANSMEM 17 37 POTENTIAL.  
 FT TRANSMEM 53 73 POTENTIAL.  
 FT TRANSMEM 135 155 POTENTIAL.  
 FT TRANSMEM 161 181 POTENTIAL.  
 FT TRANSMEM 246 266 POTENTIAL.  
 FT TRANSMEM 275 295 POTENTIAL.  
 FT NP\_BIND 370 377 ATP (POTENTIAL).  
 SQ SEQUENCE 575 AA; 64509 MW; FFI7B481DF22A0BF CRC64;

Query Match 2.9%; Score 8; DB 1; Length 575;  
 Best Local Similarity 100.0%; Pred. No. 6.6;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 232 ATLALYL 239  
 |||||  
 DB 160 ATLALYL 167

RESULT 9  
 TREA\_RABIT STANDARD; PRT; 578 AA.  
 AC P19813;

GN	TREH OR TREH.
OS	Homo sapiens (Human).
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX	NCBI_TaxID=9606;
RN	[1]
RP	SEQUENCE FROM N.A.
RC	TISSUE=Kidney;
RX	MEDLINE=98087419; PubMed=9427547;
RA	Ishihara R., Taketani S., Sasai-Takedatsu M., Kino M., Tokunaga R.,
RT	Kobayashi Y.,
RT	"Molecular cloning, sequencing and expression of cDNA encoding human
RL	trehalase.";
RN	Gene 202:69-74(1997).
RP	[2]
RC	PARTIAL SEQUENCE
RX	MEDLINE=96369335; PubMed=8773341;
RA	Sasai-Takedatsu M., Taketani S., Nagata N., Furukawa T., Tokunaga R.,
RT	Kojima T., Kobayashi Y.;
RT	"Human trehalase: characterization, localization, and its increase in
RL	urine by renal proximal tubular damage.";
CC	Nephron 73:179-185(1996).
CC	-1- FUNCTION: INTESTINAL TREHALASE IS PROBABLY INVOLVED IN THE
CC	HYDROLYSIS OF INGESTED TREHALOSE.
CC	-1- CATALYTIC ACTIVITY: Alpha,alpha-trehalose + H(2)O -> 2 D-glucose.
CC	-1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED (BY SIMILARITY).
CC	-1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
CC	-1- SIMILARITY: BELONGS TO FAMILY 37 OF GLYCOSYL HYDROLASES.
CC	-----
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CC	or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).
CC	-----
DR	EMBL; AB000824; BAA24381.1; -
DR	MIM; 273360; -
DR	InterPro; IPR001661; Trehalase.
DR	Pfam; PF01204; Trehalase; 1.
DR	PRINTS; PR00744; GLHYDRASE37.
DR	PROSITE; PS00927; TREHALASE_1; 1.
DR	PROSITE; PS00928; TREHALASE_2; 1.
KW	Hydrolase; Glycosidase; Glycoprotein; Signal; GPI-anchor.
FT	SIGNAL 1 19
FT	CHAIN 20 559
FT	PROPEP 560 583
FT	LIPID 559 559
FT	CARBOHYD 78 78
FT	CARBOHYD 239 239
FT	CARBOHYD 261 261
FT	CARBOHYD 369 369
SO	SEQUENCE 583 AA; 66596 MW; 3EE4D31BD4D243A9 CRC64;
QY	16 LLLGLGL 23
Db	11 LLLGLGL 18
RESULT 11	
NUML_BRAJA	STANDARD: PRT; 91 AA.
AC 079420; 047424;	
DT 15-DEC-1998 (Rel. 37, Created)	
DT 15-DEC-1998 (Rel. 37, Last sequence update)	
DT 30-MAY-2000 (Rel. 39, Last annotation update)	
DE	NAOH-ubiquinone oxidoreductase chain 4L (EC 1.6.5.3).



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GN ND4L OR NAD4L OR NAD4L.
OS Branchiostoma lanceolatum (Common lancelet) (Amphioxus), and
OC Branchiostoma floridae (Florida lancelet) (Amphioxus).
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
OC Branchiostoma.
OX NCBI_TaxID=7740, 7739;
RN [1]
RP SEQUENCE FROM N.A.
RC SPECIES=Branchiostoma lanceolatum;
RX MEDLINE=96292550; PubMed=9629930;
RA Spruyt N., Delabre C., Gachein G., Laudet V.;
RT "Complete sequence of the amphioxus (Branchiostoma lanceolatum)
RT mitochondrial genome: relations to vertebrates.";
RL Nucleic Acids Res. 26:3279-3285(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC SPECIES=Branchiostoma floridae;
RX MEDLINE=99261652; PubMed=10331267;
RA Boore J.L., Daehler L.L., Brown W.M.;
RT "Complete sequence, gene arrangement, and genetic code of
RT mitochondrial DNA of the cephalochordate Branchiostoma floridae
RT (Amphioxus).";
RL Mol. Biol. Evol. 16:410-418(1999).
CC -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC
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CC
DR EMBL: Y16474; CAA76255.1; -.
DR EMBL: AF098298; AAB87993.2; -.
DR InterPro: IPR003214; Mt_NADHUb_oxidoreductase_4L.
DR Pfam: PF00420; oxidored_q2; 1.
DR ProDom: PD000359; Mt_NADHUb_oxidoreductase_4L; 1.
KW Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ SEQUENCE 91 AA; 9751 MW; 7E7D093F02468BD3 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 91;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 18 LGLGLS 24
|111111|
Db 12 LGLGLS 18

RESULT 12
GRO_MOUSE STANDARD; PRT; 96 AA.
AC P12850;
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Growth regulated protein precursor (Platelet-derived growth factor-
DE inducible protein KC) (Secretory protein N51).
GN SCVB1 OR GRO1 OR GRO OR MGSA.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=69139485; PubMed=2917992;
RX Oquendo P., Alberta J., Wen D., Graycar J.L., Derynck R., Stiles C.D.;
RA "The platelet-derived growth factor-inducible KC gene encodes a
RT secretory protein related to platelet alpha-granule proteins.";

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RL J. Biol. Chem. 264:4133-4137(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89078502; PubMed=2909392;
RA Ryseck R.P., Macdonald-Bravo H., Mallet M.-G., Bravo R.;
RT "Cloning and sequence of a secretory protein induced by growth
RT factors in mouse fibroblasts.";
RL Exp. Cell Res. 180:266-275(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Bozic C.R., Kolakowski L.F. Jr., von Uexkull C., Garcia-Rodriguez M.,
RA Conklyn M.J., Breslow R., Shewell H.J., Gerard N.P., Gerard C.;
RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE OF 1-10 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=96016008; PubMed=7561058;
RA Ohmori Y., Fukumoto S., Hamilton T.A.;
RT "Two structurally distinct kappa B sequence motifs cooperatively
RT control LPS-induced KC gene transcription in mouse macrophages.";
RL J. Immunol. 155:3593-3600(1995).
CC -1- FUNCTION: HAS CHEMOTACTIC ACTIVITY FOR NEUTROPHILS. CONTRIBUTES TO
CC NEUTROPHIL ACTIVATION DURING INFLAMMATION (BY SIMILARITY).
CC -1- INDUCTION: BY PLATELET-DERIVED GROWTH FACTOR. IN LUNG, BY
CC LIPOLYSACCHARIDE OR INFLAMMATION (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE
CC C-X-C) (CHEMOKINE CXC).
CC
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CC
DR EMBL: J04596; AAA40131.1; -.
DR EMBL: U20634; AAB03376.1; -.
DR EMBL: U20527; AAB03376.1; JOINED.
DR EMBL: S79767; -. NOT_ANNOTATED_CDS.
DR PIR: A32954; A32954.
DR PIR: JH0081; JH0081.
DR HSSP: P19875; 10NK.
DR MGD: MGI:108068; Grol.
DR InterPro: IPR001811; Chemokine_IL8.
DR InterPro: IPR001089; Small_cytokine_CXC.
DR Pfam: PF00048; IL8; 1.
DR PRINTS: PR00437; SMALLCYTRCXC.
DR SMART: SM00199; SCY; 1.
DR PROSITE: PS00471; SMALL_CYTOKINES_CXC; 1.
KW Cytokine; Growth factor; Inflammatory response; Signal.
FT SIGNAL 1 24 PROBABLE.
FT CHAIN 1 96 GROWTH REGULATED PROTEIN.
FT DISULFID 33 59 BY SIMILARITY.
FT DISULFID 35 75 BY SIMILARITY.
SQ SEQUENCE 96 AA; 10254 MW; 4A52B5E5C38BA5C2 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 96;
Best Local Similarity 100.0%; Pred. No. 13;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 CAALLL 19
|111111|
Db 10 CAALLL 16

RESULT 13
ELAB_ECOLI STANDARD; PRT; 101 AA.
AC P52084; Q47010;
DT 01-OCT-1996 (Rel. 34, Created)

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DT 01-NOV-1997 (Rel. 35, last sequence update)  
 DT 16-OCT-2001 (Rel. 40, last annotation update)  
 DE Elab protein.  
 GN ELAB OR B2266 OR Z3526 OR ECS3154.  
 OS Escherichia coli. and  
 OS Escherichia coli O157:H7.  
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;  
 OC Escherichia.  
 OX NCBI\_TaxID=562, 83334;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RA Hulsmann G.W.;  
 RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MG1655;  
 RX MEDLINE=97426617; PubMed=9278503;  
 RA Blattner F.R., Plunkett G., III, Bloch C.A., Perna N.T., Burland V.,  
 RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,  
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,  
 RA Mau B., Shao Y.;  
 RT "The complete genome sequence of Escherichia coli K-12."  
 RL Science 277:1453-1474 (1997).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12;  
 RX MEDLINE=97349980; PubMed=9205837;  
 RA Yamamoto Y., Alba H., Baba T., Hayashi K., Inada T., Isono K.,  
 RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsuhashi N.,  
 RA Mizubuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,  
 RA Oshima T., Oyama S., Saito N., Stampel G., Satoh Y., Sivasubraman S.,  
 RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,  
 RA Yamagata S., Horiiuchi T.;  
 RT "Construction of a contiguous 874-Kb sequence of the Escherichia coli  
 RT - K12 genome corresponding to 50.0-68.8 min on the linkage map and  
 RT analysis of its sequence features."  
 RL DNA Res. 4:91-113 (1997).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-K12 / MC4100;  
 RX MEDLINE=96410724; PubMed=8549818;  
 RA Mueller R., Dahm C., Schulte G., Leitner E.;  
 RT "An isochlorismate hydroxymutase isogene in Escherichia coli."  
 RL PEBB Lett. 378:131-134 (1996).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / EDL933 / ATCC 700927;  
 RX MEDLINE=21074935; PubMed=11206551;  
 RA Perna N.T., Plunkett G., III, Burland V., Mau B., Glasner J.D.,  
 RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,  
 RA Postel G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,  
 RA Grobbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,  
 RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,  
 RA Welch R.A., Blattner F.R.;  
 RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7."  
 RL Nature 409:529-533 (2001).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-O157:H7 / RIMD 0509952;  
 RX MEDLINE=21156231; PubMed=11258796;  
 RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,  
 RA Han C.-G., Ohnishi E., Nakayama K., Murata T., Tanaka M., Tobe T.,  
 RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,  
 RA Kuhara S., Shiba T., Hattori M., Shinagawa H.;  
 RT "Complete genome sequence of enterohaemorrhagic Escherichia coli  
 RT O157:H7 and genomic comparison with a laboratory strain K-12."  
 RL DNA Res. 8:111-221 (2001).  
 RN [7]  
 RP IDENTIFICATION.  
 RA Rudd K.E.;  
 RL Unpublished observations (MAR-1996).  
 CC -1- SIMILARITY: STRONG, TO E.COLI YGAM AND YGJD.

CC -1- CAUTION: REF. 4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A  
 CC FRAMESHIFT IN POSITION 73.  
 CC -----  
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 CC -----  
 DR EMBL: U58768; AAB02730.1; -  
 DR EMBL: AE000316; AAC75326.1; -  
 DR EMBL: D90858; CAB22026.1; -  
 DR EMBL: D90857; CAB22016.1; -  
 DR EMBL: Z50849; -; NOT\_ANNOTATED\_CDS.  
 DR EMBL: AE005459; AAG57399.1; -  
 DR EMBL: AP002561; BAB36577.1; -  
 DR Ecocore: EG13185; elab.  
 KW Complete proteome.  
 SQ SEQUENCE 101 AA; 11306 MW; B934E815C373CF6F CRC64;

QY Query Match 2.5%; Score 7; DB 1; Length 101;  
 Db Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 222 GVLGGL 228  
 Db 91 GVLGGL 97

RESULT 14  
 H1B\_PLADU STANDARD; PRT: 119 AA.  
 ID H1B\_PLADU  
 AC P06895;  
 DT 01-JAN-1988 (Rel. 06, Created)  
 DT 01-JAN-1988 (Rel. 06, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Histone H1B, sperm.  
 OS Platynereis dumerilii (Dumeril's clam worm).  
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Palpata; Aciculata;  
 OC Phyllococida; Nereididae; Platynereis.  
 OX NCBI\_TaxID=6359;  
 RN [1]  
 RP SEQUENCE.  
 RX MEDLINE=85257663; PubMed=4018088;  
 RA Kmiecik D., Sellas D., Belachic D., Sautiere P.;  
 RT "Primary structure of the two variants of a sperm-specific histone H1  
 RT from the annelid Platynereis dumerilii."  
 RL Eur. J. Biochem. 150:359-370 (1985).  
 CC -1- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF  
 CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.  
 CC -1- SUBCELLULAR LOCATION: Nuclear.  
 CC -1- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.  
 DR PIR: B24560; HSDIB.  
 DR HSP: P02259; HST.  
 DR InterPro: IPR001386; Linker\_histone.  
 DR InterPro: IPR003216; Linkerhist\_N.  
 DR Pfam: PF00538; Linker\_histone\_1.  
 DR ProDom: PD000373; Linkerhist\_N\_1.  
 DR SMART: SM00526; H15; 1.  
 KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;  
 KW Sperm.  
 FT DOMAIN 7 77 GLOBULAR.  
 SQ SEQUENCE 119 AA; 13099 MW; CA18E93EE5963858 CRC64;

QY Query Match 2.5%; Score 7; DB 1; Length 119;  
 Best Local Similarity 100.0%; Pred. No. 16;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 215 VAAITGL 221

Db 17 VAAITGL 23

RESULT 15  
CYTF\_MOUSE

ID CYTF\_MOUSE STANDARD; PRT; 144 AA.

AC 089098;

DT 15-DEC-1998 (Rel. 37, Created)

DT 15-DEC-1998 (Rel. 37, Last sequence update)

DT 01-MAR-2002 (Rel. 41, Last annotation update)

DE Cystatin F precursor (leukocystatin) (Cystatin 7) (Cystatin-like

metastasis-associated protein) (CMAP).

GN CST7.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RA MEDLINE=98298157; PubMed=9632704;

RA Halfon S., Ford J., Foster J., Dowling L., Lucian L., Sterling M.,

RA Xu Y., Weiss M., Ikeda M., Liggert D., Helms A., Caux C., Lebecque S.,

RA Hannum C., Menon S., McClanahan T., Gorman D., Zurawski G.;

RT "Leukocystatin, a new class II cystatin expressed selectively by

hematopoietic cells."

RL J. Biol. Chem. 273:16400-16408(1998).

CC -1- FUNCTION: INHIBITS PAPAIN AND CATHEPSIN 1. BUT WITH AFFINITIES

LOWER THAN OTHER CYSTATINS. MAY PLAY A ROLE IN IMMUNE REGULATION

THROUGH INHIBITION OF A UNIQUE TARGET IN THE HEMATOPOIETIC SYSTEM.

CC -1- SUBCELLULAR LOCATION: Secreted (Probable).

CC -1- SIMILARITY: BELONGS TO THE CYSTATIN FAMILY.

CC -----

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CC -----

DR EMBL; AF031826; AAC40140.1; -

DR EMBL; AF031825; AAC40139.1; -

DR HSSP; P01038; 1A90.

DR MGD; MGI:1298217; Cst7.

DR InterPro: IPR000010; Cystatin.

DR InterPro: IPR003243; Cystatin\_C\_M.

DR Pfam; PF000031; Cystatin; 1.

DR SMART; SM00043; CY; 1.

DR PROSITE; PS00287; CYSTATIN; FALSE.NEG.

KW Thiol protease inhibitor; Glycoprotein; Signal.

FT SIGNAL 1 18 POTENTIAL.

FT CHAIN 19 144 CYSTATIN F.

FT ACT\_SITE 36 36 REACTIVE SITE.

FT SITE 80 84 SECONDARY AREA OF CONTACT.

FT DISULFID 98 109 BY SIMILARITY.

FT DISULFID 123 143 BY SIMILARITY.

SO SEQUENCE 144 AA; 16380 MW; B5837334C1B4A89C CRC64;

Query Match 2.5%; Score 7; DB 1; Length 144;

Best Local Similarity 100.0%; Pred. No. 19;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 231 LAITLAL 237

Db 3 LAITLAL 9

RESULT 16

PRI2\_HORVU

STANDARD; PRT; 164 AA.

AC P35792;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Pathogenesis-related protein PR1-2 precursor.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI\_TaxID=4513;

RN [1]

RP SEQUENCE FROM N.A.

RA STRAIN=CV. PSARKON RESISTANT; TISSUE=Leaf;

RA MEDLINE=95036024; PubMed=7524728;

RA Mouradov A., Mouradova E., Scott K.J.;

RT "Gene family encoding basic pathogenesis-related 1 proteins in

barley."

RL Plant Mol. Biol. 26:503-507(1994).

CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS

AGAINST PATHOGENS.

CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/TPX1;

INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.

CC -----

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CC -----

DR EMBL; Z26320; CAA81229.1; -

DR PIR; S37188; S37188.

DR HSSP; P04284; ICEE.

DR InterPro: IPR001283; SCP.

DR Pfam; PF00188; SCP; 1.

DR PRINTS; PR00837; V5TPXLIKE.

DR SMART; SM00198; SCP; 1.

DR PROSITE; PS01009; SCP\_AG5\_PRL\_SC7\_1;

DR PROSITE; PS01010; SCP\_AG5\_PRL\_SC7\_2; 1.

KW pathogenesis-related protein; Signal; Multigene family.

FT SIGNAL 1 24 BY SIMILARITY.

FT CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN PR1-2.

FT MOD\_RES 25 25 PYROLIDONE CARBOXYLIC ACID

FT DISULFID 68 140 (BY SIMILARITY).

FT DISULFID 113 119 BY SIMILARITY.

FT DISULFID 135 150 BY SIMILARITY.

SO SEQUENCE 164 AA; 17679 MW; DDB722DB74EEF390 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 164;

Best Local Similarity 100.0%; Pred. No. 21;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 231 LAITLAL 237

Db 6 LAITLAL 12

RESULT 17

PRI1\_HORVU

STANDARD; PRT; 164 AA.

ID PRI1\_HORVU

AC 005968;

DT 01-JUN-1994 (Rel. 29, Created)

DT 01-JUN-1994 (Rel. 29, Last sequence update)

DT 01-NOV-1997 (Rel. 35, Last annotation update)

DE Pathogenesis-related protein 1 precursor.

OS Hordeum vulgare (Barley).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;

OC Triticeae; Hordeum.

OX NCBI\_TaxID=4513;

```

RM [1]
RM SEQUENCE FROM N.A.
RX MEDLINE-94033324; PubMed-8219079;
RA Muradov A., Petrisovits L., Davidson A., Scott K.J.;
RT "A cDNA clone for a pathogenesis-related protein 1 from barley.";
RL Plant Mol. Biol. 23:439-442(1993).
CC -1- FUNCTION: PROBABLY INVOLVED IN THE DEFENSE REACTION OF PLANTS
CC AGAINST PATHOGENS.
CC -1- SIMILARITY: BELONGS TO A FAMILY THAT GROUPS MAMMALIAN SCP/PPX1;
CC INSECTS AG3/AG5; FUNGI SC7/SC14 AND PLANTS PR-1.
CC -----
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CC -----
DR EMBL: Z21494; CAA79703.1; -
DR PIR: S32002; S32002.
DR PIR: S39474; S39474.
DR HSSP: P04284; ICPE.
DR InterPro: IPR001283; SCP.
DR Pfam: PF00188; SCP.1.
DR PRINTS: PR00837; V5TPXLIKE.
DR SMART: SM00198; SCP.1.
DR PROSITE: PS01009; SCP_AG5_PRI_SC7_1; 1.
DR PROSITE: PS01010; SCP_AG5_PRI_SC7_2; 1.
DR Pathogenesis-related protein: Signal; Multigene family.
FT SIGNAL 1 24 BY SIMILARITY.
FT CHAIN 25 164 PATHOGENESIS-RELATED PROTEIN 1.
FT MOD_RES 25 25 PYROLIDONE CARBOXYLIC ACID
FT FT
FT DISULFID 68 140 (BY SIMILARITY).
FT DISULFID 113 119 BY SIMILARITY.
FT DISULFID 135 150 BY SIMILARITY.
SQ SEQUENCE 164 AA; 17683 MW; 80972FF654F77395 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 164;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 231 LALLAL 237
DB 6 LALLAL 12

RESULT 18
GRAM_MOUSE STANDARD: PRT: 173 AA.
AC P51437;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Cathelin-related antimicrobial peptide precursor (Cramp) (Cathelin-
DE like protein) (CLP).
GN CNLP OR CRAMP.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;

[1]
RP SEQUENCE FROM N.A.
RX STRAIN-BALB/C; TISSUE=Bone marrow;
RA MEDLINE-96326596; PubMed-8706928;
RA Popuueva A.V., Zinovjeva M.V., Vlaser Y.W.M., Fibbe W.E.,
RA Belyavsky A.V.;
RT "A novel murine cathelin-like protein expressed in bone marrow.";
RL FEBS Lett. 391:5-8(1996).
CC [13]
CC SEQUENCE FROM N.A.
CC STRAIN-129/SVJ;
CC Hutterer K.M., Pitrano J., Gallo R.L.;
CC Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ACTS AS A POTENT ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND
CC INTERSTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL
CC MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.
CC -1- SIMILARITY: BELONGS TO THE CATHELICIDINS FAMILY.
CC -----
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CC -----
DR EMBL: U43409; AAA85898.1; -
DR EMBL: X94353; CAA64078.1; -
DR EMBL: AF035680; AAB88303.1; -
DR HSSP: P25230; ILVP.
DR MGD: MGI:108443; CNLP.
DR InterPro: IPR001894; Cathelicidin.
DR Pfam: PF00666; Cathelicidins; 1.
DR ProDom: PD001838; Cathelicidin; 1.
DR PROSITE: PS00946; CATHELICIDINS_1; 1.
DR PROSITE: PS00947; CATHELICIDINS_2; 1.
DR Antibiotic: Signal.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 139 POTENTIAL.
FT CHAIN 140 173 CATHELIN-RELATED ANTIMICROBIAL PEPTIDE.
FT MOD_RES 28 28 PYROLIDONE CARBOXYLIC ACID (BY
FT FT
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 105 122 BY SIMILARITY.
FT CONFLICT 24 24 L->M (IN REF. 2).
FT CONFLICT 173 173 MISSING (IN REF. 1).
SQ SEQUENCE 173 AA; 19581 MW; 143F0E784762E77E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLSLG 22
DB 19 LLLSLG 25

RESULT 19
NU6M_ONCMY STANDARD: PRT: 173 AA.
ID NU6M_ONCMY
AC P48177;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
GN MTND6 OR ND6.
OS Oncoerychnus mykiss (Rainbow trout) (Salmo gairdneri).
OC Euteleostomi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

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RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Bone marrow;
RX MEDLINE-96326596; PubMed-8706928;
RA Popuueva A.V., Zinovjeva M.V., Vlaser Y.W.M., Fibbe W.E.,
RA Belyavsky A.V.;
RT "A novel murine cathelin-like protein expressed in bone marrow.";
RL FEBS Lett. 391:5-8(1996).
CC [13]
CC SEQUENCE FROM N.A.
CC STRAIN-129/SVJ;
CC Hutterer K.M., Pitrano J., Gallo R.L.;
CC Submitted (DEC-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: ACTS AS A POTENT ANTIMICROBIAL PEPTIDE.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN TESTIS, SPLEEN, STOMACH, AND
CC INTERSTINE. VERY LOW EXPRESSION FOUND IN HEART, LUNG AND SKELETAL
CC MUSCLE. NO EXPRESSION IN BRAIN, KIDNEY OR LIVER.
CC -1- SIMILARITY: BELONGS TO THE CATHELICIDINS FAMILY.
CC -----
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CC -----
DR EMBL: U43409; AAA85898.1; -
DR EMBL: X94353; CAA64078.1; -
DR EMBL: AF035680; AAB88303.1; -
DR HSSP: P25230; ILVP.
DR MGD: MGI:108443; CNLP.
DR InterPro: IPR001894; Cathelicidin.
DR Pfam: PF00666; Cathelicidins; 1.
DR ProDom: PD001838; Cathelicidin; 1.
DR PROSITE: PS00946; CATHELICIDINS_1; 1.
DR PROSITE: PS00947; CATHELICIDINS_2; 1.
DR Antibiotic: Signal.
FT SIGNAL 1 27 POTENTIAL.
FT PROPEP 28 139 POTENTIAL.
FT CHAIN 140 173 CATHELIN-RELATED ANTIMICROBIAL PEPTIDE.
FT MOD_RES 28 28 PYROLIDONE CARBOXYLIC ACID (BY
FT FT
FT DISULFID 83 94 BY SIMILARITY.
FT DISULFID 105 122 BY SIMILARITY.
FT CONFLICT 24 24 L->M (IN REF. 2).
FT CONFLICT 173 173 MISSING (IN REF. 1).
SQ SEQUENCE 173 AA; 19581 MW; 143F0E784762E77E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLSLG 22
DB 19 LLLSLG 25

RESULT 19
NU6M_ONCMY STANDARD: PRT: 173 AA.
ID NU6M_ONCMY
AC P48177;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
GN MTND6 OR ND6.
OS Oncoerychnus mykiss (Rainbow trout) (Salmo gairdneri).
OC Euteleostomi.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
OX NCBI_TaxID=8022;

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RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=96139027; PubMed=8587139;
RA      Zardoya R., Garrido-Perterra A., Bautista J.M.;
RT      "The complete nucleotide sequence of the mitochondrial DNA genome of
RL      J. Mol. Evol. 41:942-951(1995).
CC      -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC      -----
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CC      -----
DR      EMBL; L29771; AAB03358.1; -
DR      InterPro; IPR001457; Oxidored_q3.
DR      Pfam; PF00499; oxidored_q3; 1.
KM      Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ      SEQUENCE 173 AA; 18144 MW; A02134BC15D0C3F CRC64;

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Query Match          2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      221 LGVLGL 227
        |||||
Db      10 LGVLGL 16

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RESULT 20
ID      N06M_SALSA STANDARD; PRT; 173 AA.
AC      Q92ZM2;
DT      30-MAY-2000 (Rel. 39, Created)
DT      30-MAY-2000 (Rel. 39, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      NADH-ubiquinone oxidoreductase chain 6 (EC 1.6.5.3).
GN      NMD6 OR ND6 OR NADH6 OR NADH-6.
OS      Salmo salar (Atlantic salmon).
OC      Mitochondrion.
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC      Protacanthopterygii; Salmoniformes; Salmonidae; Salmo.
OX      NCBI_TaxID=8030;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Liver;
RX      MEDLINE=20018174; PubMed=10548724;
RA      Hurst C.D., Bartlett S.E., Davidson W.S., Bruce I.J.;
RT      "The complete mitochondrial DNA sequence of the Atlantic salmon, Salmo
RL      salar.";
RL      Gene 239:237-242(1999).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      Arnason U., Johnson E., Rasmussen A.S.;
RT      "The complete mitochondrial genome sequence of a teleost, Salmo salar,
RL      and comparisons with other salmoniformes.";
RL      Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.
CC      -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC      -----
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR      EMBL; U12143; AAD04744.1; -
DR      EMBL; AF133701; AAF61389.1; -
DR      InterPro; IPR001457; Oxidored_q3.
DR      Pfam; PF00499; oxidored_q3; 1.
KM      Oxidoreductase; NAD; Ubiquinone; Mitochondrion.
SQ      SEQUENCE 173 AA; 18388 MW; 55322B94E97CE17 CRC64;

```

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Query Match          2.5%; Score 7; DB 1; Length 173;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      221 LGVLGL 227
        |||||
Db      10 LGVLGL 16

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RESULT 21
ID      N00A_PARDE STANDARD; PRT; 200 AA.
AC      P29922;
DT      01-APR-1993 (Rel. 25, Created)
DT      01-APR-1993 (Rel. 25, Last sequence update)
DT      01-NOV-1995 (Rel. 32, Last annotation update)
DE      NADH-ubiquinone oxidoreductase chain 10 (EC 1.6.5.3) (NADH
DE      dehydrogenase 1, chain 10) (NDH-1, chain 10).
GN      NQO10.
OS      Paracoccus denitrificans.
OC      Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
OC      Paracoccus.
OX      NCBI_TaxID=266;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=ATCC 13543;
RX      MEDLINE=93136200; PubMed=8422400;
RA      Xu X., Matsuno-Yagi A., Yagi T.;
RT      "DNA sequencing of the seven remaining structural genes of the gene
RT      cluster encoding the energy-transducing NADH-quinone oxidoreductase
RL      of Paracoccus denitrificans.";
RL      Biochemistry 32:968-981(1993).
CC      -1- CATALYTIC ACTIVITY: NADH + ubiquinone = NAD(+) + ubiquinol.
CC      -1- SUBUNIT: COMPOSED OF 14 DIFFERENT SUBUNITS. SUBUNITS N007-14
CC      CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC      -1- SIMILARITY: TO POLYPEPTIDE 6 OF THE NADH-UBIQUINOL OXIDOREDUCTASE
CC      OF CHLOROPLASTS OR MITOCHONDRIA.
CC      -----

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DR      EMBL; L02354; AAA25596.1; -
DR      PIR; F45456;
DR      InterPro; IPR001457; Oxidored_q3.
DR      Pfam; PF00499; oxidored_q3; 1.
KM      Oxidoreductase; NAD; Ubiquinone; Transmembrane.
RN      [1]
RP      TRANSMEM 22
FT      TRANSMEM 26 46 POTENTIAL.
FT      TRANSMEM 51 71 POTENTIAL.
FT      TRANSMEM 90 110 POTENTIAL.
FT      TRANSMEM 144 164 POTENTIAL.
SQ      SEQUENCE 200 AA; 21819 MW; 903B421C3F4ACAE CRC64;

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Query Match          2.5%; Score 7; DB 1; Length 200;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      219 LGVLGL 225

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DB      133 LGGLVGL 139

RESULT  22
HA2Q_HUMAN STANDARD: PRT: 260 AA.
ID      HA2Q_HUMAN
AC      P20036; P01905;
DT      21-JUL-1986 (Rel. 01, Created)
DT      01-FEB-1991 (Rel. 17, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      HLA class II histocompatibility antigen, DP alpha chain precursor
DE      (HLA-DP alpha chain) (MHC class II DP3-alpha) (DP(M4)).
GN      HLA-DPA1 OR HLA-SB.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=86041930; PubMed=2997750;
RA      Lawrence S.K., Das H.K., Pan J., Weissman S.M.;
RT      "The genomic organisation and nucleotide sequence of the HLA-SB(DP)
RT      alpha gene.";
RL      Nucleic Acids Res. 13:7515-7528(1985).
RN      [2]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=87250502; PubMed=3036829;
RA      Gustafsson K., Widmark E., Jonsson A.-K., Serenius B., Sachs D.H.,
RA      Larhammar D., Raak L., Peterson P.A.;
RT      "Class II genes of the human major histocompatibility complex.
RT      Evolution of the DP region as deduced from nucleotide sequences of
RT      the four genes.";
RL      J. Biol. Chem. 262:8778-8786(1987).
RN      [3]
RP      SEQUENCE FROM N.A.
RA      MEDLINE=89053719; PubMed=2461352;
RA      Young J.A., Lindsay J., Bodmer J.G., Trowsdale J.;
RT      "Epitope recognition by a DP alpha chain-specific monoclonal antibody
RT      (DP11.1) is influenced by the interaction between the DP alpha chain
RT      and its polymorphic DP beta chain partner.";
RL      Hum. Immunol. 23:37-44(1988).
RN      [4]
RP      SEQUENCE OF 28-260 FROM N.A.
RA      MEDLINE=84168117; PubMed=6584734;
RA      Aulfray C., Lillie J.W., Arnott D., Grossberger D., Kappes D.,
RA      Strominger J.L.;
RT      "Isotypic and allotypic variation of human class II
RT      histocompatibility antigen alpha-chain genes.";
RL      Nature 308:327-333(1984).
CC      -----
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CC      -----
DR      EMBL: X03100; CAA26887.1; -
DR      EMBL: M27487; AAA63220.1; -
DR      EMBL: X00457; CAA25143.1; -
DR      PIR: A02209; HLHUSB.
DR      PIR: A29313; A29313.
DR      HSSP: F01903; 2SEB.
DR      MIM: 142880; -
DR      InterPro: IPR003006; Ig_MHC.
DR      InterPro: IPR003587; Ig_cl.
DR      InterPro: IPR001003; MHC_II_alpha.
DR      Pfam: PF00047; Ig_1.
DR      Pfam: PF00993; MHC_II_alpha; 1.
DR      SMART: SM00407; IGCL; 1.
DR      PROSITE: PS00290; IG_MHC; 1.

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KM      MHC II: Transmembrane; Glycoprotein; Signal.
FT      SIGNAL 1 28
FT      CHAIN 29 260
FT      DOMAIN 29 115
FT      DOMAIN 116 209
FT      DOMAIN 210 222
FT      TRANSMEM 223 245
FT      DOMAIN 246 260
FT      DISULFID 138 194
FT      CAROHYD 109 109
FT      CAROHYD 149 149
FT      CONFLICT 237 237
SQ      SEQUENCE 260 AA; 29380 MM; 82617AE963A8CB42 CRC64;

Query Match      2.5%; Score 7; DB 1; Length 260;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      221 LGGLVGL 227
      . 1111111
DB      228 LGGLVGL 234

RESULT  23
BXBL_HAEIN STANDARD: PRT: 265 AA.
ID      BXBL_HAEIN
AC      P19390;
DT      01-NOV-1990 (Rel. 16, Created)
DT      01-NOV-1990 (Rel. 16, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Capsule polysaccharide export inner-membrane protein bexb.
GN      BEXB.
OS      Haemophilus influenzae.
OC      Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
OC      Haemophilus.
OX      NCBI_TaxID=727;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      STRAIN=RM 153 / SEROTYPE B;
RA      MEDLINE=90170850; PubMed=2137816;
RA      Kroll J.S., Moxon E.R.;
RT      "Capsulation in distantly related strains of Haemophilus influenzae
RT      type b: genetic split and gene transfer at the capsulation locus.";
RL      J. Bacteriol. 172:1374-1379(1990).
CC      -1- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT
CC      APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC      (potential).
CC      -1- SIMILARITY: BELONGS TO THE ABC-2 SUBFAMILY OF INTEGRAL MEMBRANE
CC      PROTEINS.
CC      -1- SIMILARITY: 95% IDENTITY TO RM926 BEXB.
CC      -----
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CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: M33787; AAA24945.1; -
DR      InterPro: IPR000412; ABC2_transport.
DR      Pfam: PFO1061; ABC2_membrane; 1.
DR      PRINTS: PR00164; ABC2TRANSPO.
DR      PROSITE: PS00890; ABC2_MEMBRANE; 1.
KM      Polysaccharide transport; Transmembrane; Inner membrane.
FT      TRANSMEM 37 57
FT      TRANSMEM 64 84
FT      TRANSMEM 118 138
FT      TRANSMEM 151 171
FT      TRANSMEM 176 198

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FT TRANSMEM 235 255 POTENTIAL.  
SQ SEQUENCE 265 AA; 30181 MW; 0A436F824CD25C1 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLGL 21  
|||||||  
Db 246 ALLLGL 252

RESULT 24  
BXB3\_HAEIN  
ID BXB3\_HAEIN STANDARD; PRT; 265 AA.  
AC P22235;  
DT 01-AUG-1991 (Rel. 19, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 16-OCT-2001 (Rel. 40, Last annotation update)  
DE Capsule polysaccharide export inner-membrane protein bexB.  
GN BXB3.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OX Haemophilus.  
OX NCBI\_Taxid=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=EAGAN / SEROTYPE B;  
RX MEDLINE=91186821; PubMed=2082145;  
RA Kroll J.S., Loynds B., Brophy L.N., Moxon E.R.;  
RT "The bex locus in encapsulated Haemophilus influenzae: a chromosomal  
RT region involved in capsule polysaccharide export.";  
RL Mol. Microbiol. 4:1853-1862(1990).  
CC -1- FUNCTION: MAY FORM AN ATP-DRIVEN CAPSULE POLYSACCHARIDE EXPORT  
CC APPARATUS, IN ASSOCIATION WITH THE BEXA, BEXC AND BEXD PROTEINS.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane  
CC (Potential).  
CC -1- SIMILARITY: BELONGS TO THE ABC-2 SUBFAMILY OF INTEGRAL MEMBRANE  
CC PROTEINS.

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CC -----  
DR EMBL; X54987; CAA38733.1; -.  
DR PIR; S12234; BWHIXB.  
DR InterPro: IPR000412; ABC2\_transport.  
DR Pfam; PF01061; ABC2\_membrane; 1.  
DR PRINTS; PR00164; ABC2TRANSPORT.  
DR PROSITE; PS00890; ABC2\_MEMBRANE; 1.  
KW Polysaccharide transport; Transport; Transmembrane; Inner membrane.  
FT TRANSMEM 37 57 POTENTIAL.  
FT TRANSMEM 64 84 POTENTIAL.  
FT TRANSMEM 118 138 POTENTIAL.  
FT TRANSMEM 151 171 POTENTIAL.  
FT TRANSMEM 178 198 POTENTIAL.  
FT TRANSMEM 235 255 POTENTIAL.  
SQ SEQUENCE 265 AA; 30195 MW; E3A4F181C4B3203E CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLGL 21  
|||||||  
Db 246 ALLLGL 252

RESULT 25  
YG95\_HAEIN  
ID YG95\_HAEIN STANDARD; PRT; 267 AA.  
AC Q48215; Q05081;  
DT 16-OCT-2001 (Rel. 40, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 01-MAR-2002 (Rel. 41, Last annotation update)  
DE Putative glycosyl transferase H11695 (EC 2.-.-.-).  
GN H11695.  
OS Haemophilus influenzae.  
OC Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;  
OX Haemophilus.  
OX NCBI\_Taxid=727;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=A2;  
RA McLaughlin R., Abu Kwaik Y., Young R., Spinoia S., Apicella M.;  
RT "Characterization and sequence of the lsg locus from Haemophilus  
RT influenzae.";  
RL Submitted (JUN-1992) to the EMBL/GenBank/DBJ databases.

CC -----  
RP SEQUENCE FROM N.A.  
RC STRAIN=RD / KW20 / ATCC 51907;  
RX MEDLINE=95350630; PubMed=7542800;  
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F.,  
RA Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,  
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,  
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,  
RA Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D.,  
RA Uterlack T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C.,  
RA Fine L.D., Fritchman J.L., Fuhrmann J.L., Geophagen N.S.M.,  
RA Gresham C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,  
RA Venter J.C.;  
RT "Whole-genome random sequencing and assembly of Haemophilus influenzae  
RT Rd.";  
RL Science 269:496-512(1995).  
CC -1- SIMILARITY: BELONGS TO THE GLYCOSYLTRANSFERASE FAMILY 2.

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CC -----  
DR EMBL; M94855; AAA24983.1; -.  
DR EMBL; U32842; AAC23341.1; -.  
DR TIGR; H11695; -.  
DR InterPro: IPR001173; Glycos\_transf\_2.  
DR Pfam; PF00535; Glycos\_transf\_2; 1.  
KW Hypothetical protein; Transferase; Glycosyltransferase;  
KW Complete proteome.  
FT CONFLICT 26 26 V -> G (IN REF. 1).  
FT CONFLICT 46 46 D -> E (IN REF. 1).  
FT CONFLICT 49 49 F -> S (IN REF. 1).  
SQ SEQUENCE 267 AA; 30770 MW; A2F1A0532737D8C3 CRC64;

Query Match  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 49 GNGWYSR 55  
|||||||  
Db 205 GNGWYSR 211

RESULT 26  
LEP4\_SYNT3  
ID LEP4\_SYNT3 STANDARD; PRT; 269 AA.  
AC P72640;

```

DT 30-MAY-2000 (Rel. 39, Created)
DT 16-OCT-2001 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type 4 preprolin-like proteins leader peptide processing enzyme
DE [includes: leader peptidase (EC 3.4.99.-) (Preprolin peptidase); N-
DE methyltransferase (EC 2.1.1.-)].
GN HOPD OR SLR1120.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=1148;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneo T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Sugiyama M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Nario K., Okumura S.,
RA Shimo S., Takeuchi C., Wada T., Watanabe A., Yamada M., Yasuda M.,
RA Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. It Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -1- FUNCTION: CLEAVES TYPE-4 FIBRILLAR LEADER SEQUENCE AND METHYLATES
CC THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO KNOWN AS TYPE
CC III LEADER PEPTIDASE FAMILY.
CC -----
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CC -----
DR EMBL: D90899; BAA1642.1; .
DR MEROPS: A24.004; .
DR InterPro: IPR000045; Peptidase_C20.
DR Pfam: PF01478; Peptidase_C20; 1.
DR PRINTS: PR00864; PREPLMPRTSE.
KW Multifunctional enzyme; Hydrolase; Protease; Transferase;
KW Methyltransferase; Transmembrane; Complete proteome.
FT TRANSMEM 4 24 POTENTIAL.
FT TRANSMEM 100 120 POTENTIAL.
FT TRANSMEM 127 147 POTENTIAL.
FT TRANSMEM 154 174 POTENTIAL.
FT TRANSMEM 197 217 POTENTIAL.
FT TRANSMEM 238 258 POTENTIAL.
SO SEQUENCE 269 AA; 29767 MW; 4056E0AA9654B1C CRC64;

Query Match 2.5%; Score 7; DB 1; Length 269;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GLVLGL 228
DB 135 GLVLGL 141

RESULT 27
LEPA_ERMCH STANDARD; PRT; 283 AA.
ID LEPA_ERMCH
AC P31711;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Type 4 preprolin-like proteins leader peptide processing enzyme (Pectic
DE enzymes secretion protein outo) [includes: Leader peptidase
DE (EC 3.4.99.-) (Preprolin peptidase); N-methyltransferase (EC 2.1.1.-)].
GN OUPD.
OS Erwinia chrysanthemi.

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OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Pectobacterium.
OX NCBI_TaxID=556;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=EC16;
RX MEDLINE=93054355; PubMed=1429461;
RA Lindeberg M., Collmer A.;
RT "Analysis of eight out genes in a cluster required for pectic enzyme
RT secretion by Erwinia chrysanthemi: sequence comparison with secretion
RT genes from other Gram-negative bacteria.";
RL J. Bacteriol. 174:7385-7397(1992).
CC -1- FUNCTION: CLEAVES TYPE-4 FIBRILLAR LEADER SEQUENCE AND METHYLATES
CC THE N-TERMINAL (GENERALLY PHE) RESIDUE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY A24; ALSO KNOWN AS TYPE
CC III LEADER PEPTIDASE FAMILY.
CC -----
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CC -----
DR EMBL: L02214; AAA24841.1; .
DR PIR: C47755; C47755.
DR MEROPS: A24.001; .
DR InterPro: IPR000045; Peptidase_C20.
DR Pfam: PF01478; Peptidase_C20; 1.
DR PRINTS: PR00864; PREPLMPRTSE.
KW Multifunctional enzyme; Hydrolase; Protease; Transferase;
KW Methyltransferase; Transmembrane; Inner membrane.
FT TRANSMEM 13 33 POTENTIAL.
FT TRANSMEM 106 126 POTENTIAL.
FT TRANSMEM 128 148 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 176 196 POTENTIAL.
FT TRANSMEM 216 236 POTENTIAL.
FT TRANSMEM 259 279 POTENTIAL.
SO SEQUENCE 283 AA; 31355 MW; 90B9CE722C4AA7E CRC64;

Query Match 2.5%; Score 7; DB 1; Length 283;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ALLLGL 21
DB 17 ALLLGL 23

RESULT 28
Y635_METJA STANDARD; PRT; 283 AA.
ID Y635_METJA
AC Q58052;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein MJ0635.
GN MJ0635.
OS Methanococcus jannaschii.
OC Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
OC Methanococcus.
OX NCBI_TaxID=2190;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX MEDLINE=96337999; PubMed=8688087;
RA Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA Sutton G.G., Blake J.A., FitzGerald L.M., Clayton R.A., Gocayne J.D.,

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RA Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,  
 RA Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodok A.,  
 RA Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L., Nguyen D.,  
 RA Uterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,  
 RA Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,  
 RA Klenk H.-P., Fraser C.M., Smith H.O., Moese C.R., Venter J.C.,  
 RT "Complete genome sequence of the methanogenic archaeon, Methanococcus  
 jannaschii";  
 RL Science 273:1058-1073(1996).  
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 CC -----  
 CC EMBL; U67511; AAB98633.1; -  
 DR TIGR; MJO635; -  
 DR Hypothetical protein; Complete proteome.  
 KM SEQUENCE 283 AA; 32502 MW; 1CE52FC8457C5E20 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 283;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 231 LAIILAL 237  
 |||||  
 Db 10 LAIILAL 16

RESULT 29  
 VB1L\_CLVK STANDARD; PRT; 298 AA.  
 AC P14981;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE B1L protein (33.7 kDa protein).  
 GN BCL1.  
 OS Cassava latent virus (strain West Kenya 844).  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OX NCBI\_TaxID=10818;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Stanley J., Gay M.R.;  
 RT "Nucleotide sequence of cassava latent virus DNA.";  
 RL Nature 301:260-262(1983).  
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES B1L PROTEIN FAMILY.  
 CC -----  
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 CC -----  
 CC EMBL; J02058; -; NOT\_ANNOTATED\_CDS.  
 DR InterPro; IPR000211; Gemini1.BL.  
 DR Pfam; PF00845; Gemini1.BL; 1.  
 SO SEQUENCE 298 AA; 33773 MW; D1E37C3F3B4CFPA5 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 RPIYOP 191  
 |||||  
 Db 199 RPIYOP 205

RESULT 30  
 VB1L\_CLVN STANDARD; PRT; 298 AA.  
 AC P14971;  
 DT 01-APR-1990 (Rel. 14, Created)  
 DT 01-APR-1990 (Rel. 14, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE B1L protein (33.7 kDa protein).  
 GN BCL1.  
 OS Cassava latent virus (strain Nigerian).  
 OC Viruses; ssDNA viruses; Geminiviridae; Begomovirus.  
 OX NCBI\_TaxID=10819;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90174930; PubMed=2308831;  
 RA Morris B., Coates L., Lowe S., Richardson K., Eddy P.;  
 RT "Nucleotide sequence of the infectious cloned DNA components of  
 RT African cassava mosaic virus (Nigerian strain).";  
 RL Nucleic Acids Res. 18:197-198(1990).  
 CC -1- SIMILARITY: BELONGS TO GEMINIVIRUSES B1L PROTEIN FAMILY.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC EMBL; X17096; CAA34955.1; -  
 DR PIR; S07596; S07596.  
 DR InterPro; IPR000211; Gemini1.BL.  
 DR Pfam; PF00845; Gemini1.BL; 1.  
 SO SEQUENCE 298 AA; 33648 MW; 87C5BCE912519526 CRC64;

Query Match 2.5%; Score 7; DB 1; Length 298;  
 Best Local Similarity 100.0%; Pred. No. 35;  
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 185 RPIYOP 191  
 |||||  
 Db 199 RPIYOP 205

Search completed: June 18, 2002, 14:32:26  
 Job time: 214 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: June 18, 2002, 14:29:27 ; Search time 26.53 Seconds  
(Without alignments)  
1806.242 Million cell updates/sec

Title: US-09-852-845-2  
Perfect score: 277  
Sequence: 1 MCVGARRLGRCPCAAALLLG.....SFRTPLOEQADAHSTIAKI 277

Scoring table: OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 562222 seqs, 172994929 residues

Word size : 0

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

Database :

1: SPREMBL\_19:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mhc:\*  
9: sp\_organelle:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rodent:\*  
13: sp\_virus:\*  
14: sp\_vertebrate:\*  
15: sp\_unclassified:\*  
16: sp\_virus:\*  
17: sp\_bacteriaph:\*  
17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	17	6.1	267	6	002764
2	9	3.2	2126	11	0920T6
3	8	2.9	109	11	0920X4
4	8	2.9	151	4	09UF74
5	8	2.9	162	11	09CWE9
6	8	2.9	162	16	051707
7	8	2.9	185	7	09NFG2
8	8	2.9	191	4	09H7A9
9	8	2.9	199	16	098KM8
10	8	2.9	204	5	09NFD4
11	8	2.9	208	11	09D5A9
12	8	2.9	215	5	020614
13	8	2.9	236	7	031625
14	8	2.9	236	7	031359
15	8	2.9	250	7	031150
16	8	2.9	250	11	09QWV1

17	8	2.9	264	2	09X647	09X647 aeromonas h
18	8	2.9	282	4	09NPF0	09NPF0 homo sapien
19	8	2.9	306	2	09FDT4	09FDT4 streptolocc
20	8	2.9	315	16	099UT7	099UT7 staphylococ
21	8	2.9	329	10	043324	043324 populus x c
22	8	2.9	432	2	093J03	093J03 streptomyc
23	8	2.9	443	16	09HW78	09HW78 pseudomonas
24	8	2.9	473	11	09CY76	09CY76 mus musculu
25	8	2.9	473	16	005295	005295 mycobacteri
26	8	2.9	476	16	050017	050017 mycobacteri
27	8	2.9	513	16	097097	097097 streptococ
28	8	2.9	576	11	09JLT2	09JLT2 mus musculu
29	8	2.9	621	4	09P264	09P264 homo sapien
30	8	2.9	768	4	060279	060279 homo sapien
31	8	2.9	852	4	09H956	09H956 homo sapien
32	8	2.9	1031	10	065500	065500 arabidopsis
33	8	2.5	45	11	09ET76	09ET76 mus musculu
34	7	2.5	47	10	09FSP6	09FSP6 oryza sativ
35	7	2.5	52	8	036274	036274 zea mays (m
36	7	2.5	53	4	096IX8	096IX8 homo sapien
37	7	2.5	88	2	P71190	P71190 escherichia
38	7	2.5	93	16	09RZ65	09RZ65 deinococcus
39	7	2.5	100	12	091FS4	091FS4 chilo iride
40	7	2.5	103	16	09RWM3	09RWM3 deinooccus
41	7	2.5	105	11	0920X5	0920X5 mus musculu
42	7	2.5	105	11	091VE7	091VE7 mus musculu
43	7	2.5	113	2	045273	045273 bradyrhizob
44	7	2.5	114	5	095Q24	095Q24 caenorhabdi
45	7	2.5	115	13	090Y43	090Y43 osteoglossu
46	7	2.5	116	10	09ZSJ6	09ZSJ6 arabidopsis
47	7	2.5	116	16	09XIV2	09XIV2 thermotoga
48	7	2.5	129	9	094MT2	094MT2 bacterioph
49	7	2.5	133	16	P74742	P74742 synechocyst
50	7	2.5	139	16	09JR37	09JR37 neisseria m

# ALIGNMENTS

RESULT 1					
ID 002764	PRELIMINARY;	PRT;	267 AA.		
AC 002764:					
DT 01-JUL-1997 (TREMblrel. 04, Created)					
DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)					
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)					
DE OX40 PRECURSOR (FRAGMENT).					
OS Oryctolagus cuniculus (Rabbit).					
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.					
OX NCBI_TaxId=9986;					
RN [1]					
RP SEQUENCE FROM N.A.					
RC STRAIN=CHB:HM;					
RA Isono T., Seto A.;					
RT "Expression of OX40 and OX40 ligand genes in rabbit HTLV-I-transformed T cell lines."					
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.					
DR EMBL; AB003911; BAA20059.1; -.					
DR HSSP; P25942; 1CDF.					
DR InterPro; IPR01368; TNFR_c6.					
DR Pfam; PF00020; TNFR_c6; 3.					
DR ProDom; PD000771; TNFR_c6; 1.					
DR SMART; SM00208; TNFR_3.					
DR PROSITE; PS00852; TNFR_NGFR_1; 2.					
DR PROSITE; PS00500; TNFR_NGFR_2; 2.					
KW Signal.					
FT NON_TER	1	1			
FT SIGNAL	<1	18	POTENTIAL.		
FT CHAIN	19	267	OX40.		
SQ SEQUENCE	267 AA;	28489 MW;	ABB4CD3173C9500B CRC64;		

Query Match 6.1%; Score 17; DB 6; Length 267;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-08;  
 Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 254 PGGSFRPIQEQADA 270  
 DB 244 PGGSFRPIQEQADA 260

## RESULT 2

ID 0920T6 PRELIMINARY; PRT; 2126 AA.  
 AC 0920T6;  
 DT 01-MAY-1999 (TREMBLrel. 10, Created)  
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE POLYCYSTIC KIDNEY DISEASE AND RECEPTOR FOR EGG JELLY RELATED PROTEIN.  
 DE PROTEIN.  
 GN PKDREJ.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=99138702; PubMed=9949214;  
 RA Hughes J., Ward C.J., Aspinwall R., Butler R., Harris P.C.;  
 RT "Identification of a human homologue of the sea urchin receptor for egg jelly: a polycystic kidney disease-like protein.";  
 RL Hum. Mol. Genet. 8:543-549(1999).  
 DR EMBL; AF16455; AAD18022.1; .  
 DR MGD; MGI:138786; PKdrej.  
 DR InterPro; IPR000636; Cation\_chan\_non\_119.  
 DR InterPro; IPR002111; Cat\_channel\_Tprl.  
 DR InterPro; IPR001024; LH2.  
 DR InterPro; IPR000203; PKD\_cys\_rich.  
 DR InterPro; IPR002859; REJ.  
 DR Pfam; PF00520; Ion\_Trans; 1.  
 DR Pfam; PF01477; PLAT; 1.  
 DR Pfam; PF02010; REJ; 1.  
 DR SMART; SM00303; GPS; 1.  
 DR SMART; SM00308; LH2; 1.  
 KW Receptor.  
 SQ SEQUENCE 2126 AA; 241389 MW; AOCEDAAOD8219A84 CRC64;

Query Match 3.2%; Score 9; DB 11; Length 2126;  
 Best Local Similarity 100.0%; Pred. No. 8.9;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 15 ALLLGLGL 23  
 DB 6 ALLLGLGL 14

## RESULT 3

ID 0920X4 PRELIMINARY; PRT; 109 AA.  
 AC 0920X4;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE CAHELICIDIN (FRAGMENT).  
 DE CRAMP.  
 GN Mus spicilegus (Steppe mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10103;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA SPRIN=ZBN.  
 RA Liu Y., Kilano T., Koide T., Shirosaki T., Moriwaki K., Saitou N.;  
 RT "Conspecific Differences among Gene Genealogies of 21 Nuclear Genes of

RT Five Mus musculus subspecies."  
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB039073; BAB68597.1; .  
 FT NON\_TER  
 FT NON\_TER  
 SQ SEQUENCE 109 AA; 12230 MW; 8FE0162551AA477C CRC64;

Query Match 2.9%; Score 8; DB 11; Length 109;  
 Best Local Similarity 100.0%; Pred. No. 6.7;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23  
 DB 16 LLLGLGL 23

## RESULT 4

ID 09UF74 PRELIMINARY; PRT; 151 AA.  
 AC 09UF74;  
 DT 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)  
 DE HYPOTHETICAL 16.6 KDA PROTEIN (FRAGMENT).  
 GN DKE2P434N1535.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA TISSUE=TESTIS;  
 RA Poustea A., Klein M., Mewes H.W., Gassenhuber J., Wiemann S.;  
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AL133575; CAB63722.1; .  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 151 AA; 16584 MW; 8092E6652B311821 CRC64;

Query Match 2.9%; Score 8; DB 4; Length 151;  
 Best Local Similarity 100.0%; Pred. No. 8.9;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 LGISTVTG 28  
 DB 35 LGISTVTG 42

## RESULT 5

ID 09CWE9 PRELIMINARY; PRT; 162 AA.  
 AC 09CWE9;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 241014IK03RIK PROTEIN.  
 GN 241014IK03RIK.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC STEM CELLS;  
 RX MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gliss C., King B., Kochiwa H.,

RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,  
 RA Sakurai L.M., Staabli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Sessa T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilmink L.,  
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontuski S.,  
 RA Hayashizaki Y.,  
 RT "Functional annotation of a full-length mouse cDNA collection.",  
 RL Nature 409:685-690(2001).  
 DR EMBL: AK010803; BAB27191.1; -;  
 DR MGD: MGI:1915216; 2410141K03rik.  
 DR InterPro: IPR001878; Znf\_CCHC.  
 DR Pfam: PF00098; Zf-CCHC; 1.  
 DR SMART: SM00343; Znf\_C2HC; 1.  
 KW Zinc-finger.  
 SQ SEQUENCE 162 AA; 17758 MW; 2CCA4888DC57B78E CRC64;

Query Match 2.9%; Score 8; DB 11; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 9.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LGLVGL 23  
 DB 144 LGLVGL 151

RESULT 6  
 ID 051707 PRELIMINARY; PRT; 162 AA.  
 AC 051707;  
 DT 01-JUN-1998 (TREMblrel. 06, Created)  
 DT 01-JUN-1998 (TREMblrel. 06, Last sequence update)  
 DE COLICIN V PRODUCTION PROTEIN, PUTATIVE.  
 GN BB0766.  
 OS Borrelia burgdorferi (Lyme disease spirochete).  
 OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.  
 OX NCBI\_TaxID=139;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 35210 / B31;  
 RX MEDLINE=98065943; PubMed=9403685;  
 RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,  
 RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,  
 RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D., Hanson M.,  
 RA Peterson J., Kerlavage A.R., Quackenbush J., Salzberg S., Hanson M.,  
 van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Bowman J.,  
 RA Ueberlack T., Wathey L., McDonald L., Artach P., Bowman C.,  
 RA Garlind S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,  
 RA Smith H.O., Venter J.C.;  
 RT "Genomic sequence of a Lyme disease spirochete, Borrelia burgdorferi."  
 RL Nature 380:580-586(1997).  
 DR EMBL: AE001176; AAC67114.1; -;  
 DR TIGR: BB0766;  
 DR InterPro: IPR003825; Colicin\_V.  
 DR Pfam: PF02674; Colicin\_V; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 162 AA; 18715 MW; 7FFA560D3EBE4201 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 162;  
 Best Local Similarity 100.0%; Pred. No. 9.4;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 OY 221 LGLVGL 228  
 I|||||

DB 107 LGLVGL 114

RESULT 7  
 ID 09NF02 PRELIMINARY; PRT; 185 AA.  
 AC 09NF02;  
 DT 01-OCT-2000 (TREMblrel. 15, Created)  
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)  
 DE 01-DEC-2001 (TREMblrel. 19, Last annotation update)  
 DE HYPOTHETICAL 21.7 KDA PROTEIN (FRAGMENT).  
 OS Plasmodium falciparum.  
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
 OX NCBI\_TaxID=5833;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3D7A;  
 RX MEDLINE=97008413; PubMed=8855557;  
 RA Alano P., Silvestrini F., Roca L.;  
 RT "Structure and polymorphism of the upstream region of the pfg 27/25  
 RT gene, transcriptionally regulated in gametocytogenesis of Plasmodium  
 RT falciparum."  
 RL Mol. Biochem. Parasitol. 79:207-217(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=3D7A;  
 RX MEDLINE=20520959; PubMed=11071280;  
 RA Sallicandro P., Paglia M.G., Hashim S.O., Silvestrini F., Picci L.,  
 RA Gentile M., Mulaa F., Alano P.;  
 RT "Repetitive sequences upstream of the pfg27/25 gene determine  
 RT polymorphism in laboratory and natural lines of Plasmodium  
 RT falciparum."  
 RL Mol. Biochem. Parasitol. 110:247-257(2000).  
 DR EMBL: AJ271108; CAB93664.1; -;  
 KW Hypothetical protein.  
 FT NON\_TER  
 SQ SEQUENCE 185 AA; 21653 MW; 774285C81B10A3D0 CRC64;

Query Match 2.9%; Score 8; DB 5; Length 185;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 VAILGL 222  
 DB 31 VAILGL 38

RESULT 8  
 ID 09H7A9 PRELIMINARY; PRT; 191 AA.  
 AC 09H7A9;  
 DT 01-MAR-2001 (TREMblrel. 16, Created)  
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)  
 DE 01-MAR-2001 (TREMblrel. 16, Last annotation update)  
 DE CDNA: FLJ21104 FIS, CLONE CAS04958.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T., Matsumura K.,  
 RA Nakajima Y., Mizuno T., Morinaga M., Tanigami A., Fujiwara T., Ono T.,  
 RA Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y., Ota T., Suzuki Y.,  
 RA Oiyashi M., Nishi T., Shibahara T., Tanaka T., Nakamura Y.,  
 RA Isoigal T., Sugano S.;  
 RT "NEDO human cDNA sequencing project."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AK024757; BAB14988.1; -;  
 SQ SEQUENCE 191 AA; 20917 MW; COEBB49678F36E0B CRC64;

Query Match 2.9%; Score 8; DB 4; Length 191;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 133 FSPGDNOA 140  
|||||||  
DB 59 FSPGDNOA 66

RESULT 9  
O98KM8 PRELIMINARY; PRT: 199 AA.

AC O98KM8: 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DT 01-OCT-2001 (TREMBlrel. 18, Last annotation update)  
DE MLR1403 PROTEIN.  
GN MLR1403.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303099;  
RX MEDLINE=21082930; PubMed=11214968;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idegawa K., Ishikawa A., Kawasaki K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shlimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti.";  
RL DNA Res. 7:331-338(2000).  
DR EMBL; AP002997; BAB48786.1; -  
KM Complete proteome.  
SQ SEQUENCE 199 AA; 22658 MW; 2AF1DECDAF29AB0 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 199;  
Best Local Similarity 100.0%; Pred. No. 11;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 216 AAILGL 223  
|||||||  
DB 125 AAILGL 132

RESULT 10  
O9NFU4 PRELIMINARY; PRT: 204 AA.

AC O9NFU4: 01-OCT-2000 (TREMBlrel. 15, Created)  
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HYOTHECTICAL 23 8 KDA PROTEIN (FRAGMENT).  
OS Plasmodium falciparum.  
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.  
OX NCBI\_TaxID=5833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20520959; PubMed=11071280;  
RA Salicandro P., Paglia M.G., Hashim S.O., Silvestrini F., Picci L.,  
RA Gentile M., Mula F., Alano P.;  
RT "Repetitive sequences upstream of the pfq27/25 gene determine  
RT polymorphism in laboratory and natural lines of Plasmodium  
RT falciparum.";  
RL Mol. Biochem. Parasitol. 110:247-257(2000).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97008413; PubMed=8855557;  
RA Alano P., Silvestrini F., Roca L.;  
RT "Structure and polymorphism of the upstream region of the pfq 27/25

RT gene, transcriptionally regulated in gametocytogenesis of Plasmodium  
RT falciparum.";  
RL Mol. Biochem. Parasitol. 79:207-217(1996).  
DR EMBL; AJ271088; CAB93662.1; -  
KM Hypothetical protein.  
FT NON\_TER 1  
SQ SEQUENCE 204 AA; 23806 MW; 27145AFB71E7E731 CRC64;

Query Match 2.9%; Score 8; DB 5; Length 204;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 215 VAILGL 222  
|||||||  
DB 50 VAILGL 57

RESULT 11  
O9D5A9 PRELIMINARY; PRT: 208 AA.

AC O9D5A9: 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE 4930474F22RIK PROTEIN.  
GN 4930474F22RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=C57BL/6J; TISSUE=TESTIS;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochwa H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Queckenbush J.,  
RA Schriml L.M., Staudt F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,  
RA Blake J., Boileau D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bull C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seta T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,  
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuki S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL; AK015573; BAB29896.1; -  
DR HSSP; P00669; IBSR.  
DR MGD; MGI:1922269; 4930474F22RIK.  
DR InterPro; IPR001427; RNaseA.  
DR PRINTS; PR00794; RIBONUCLEASE.  
DR PRODOM; PD000535; RNaseA; 1.  
DR SMART; SM00092; RNase\_Pc; 1.  
SQ SEQUENCE 208 AA; 23407 MW; 383F776927F6067C CRC64;

Query Match 2.9%; Score 8; DB 11; Length 208;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGL 23  
|||||||  
DB 14 LLLGL 21

RESULT 12  
Q20614  
ID 020614 PRELIMINARY; PRT: 215 AA.  
AC 020614;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE F49E12.7 PROTEIN.  
GN F49E12.7.  
OS Caenorhabditis elegans.  
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;  
OC Rhabditidae; Peloderinae; Caenorhabditis.  
OX NCBI\_TaxID=6239;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Thomas K.;  
RL Submitted (OCT-1995) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RX MEDLINE=99069613; PubMed=9851916;  
RA none;  
RT "Genome sequence of the nematode C.elegans: A platform for  
RT investigating biology.";  
RL Science 282:2012-2018(1998).  
DR EMBL; Z66520; CAA91386.1; -;  
SQ SEQUENCE 215 AA; 24861 MW; 23352PFD0969A84C8 CRC64;

Query Match 2.9%; Score 8; DB 5; Length 215;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 230 PLATLAL 237  
Db 25 PLATLAL 32

RESULT 13  
Q31625  
ID 031625 PRELIMINARY; PRT: 236 AA.  
AC 031625;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MHC CLASS II ALPHA CHAIN.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA MEDLINE=94011091; PubMed=8406613;  
RA Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;  
RT "Zebrafish MHC class II alpha chain-encoding genes: polymorphism,  
RT expression, and function.";  
DE Immunogenetics 38:408-420(1993).  
GN H2-OA OR H-2OA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-B10.M; TISSUE=SPLEEN;  
RX MEDLINE=92364550; PubMed=1354242;  
RA Karlsson L., Peterson P.A.;  
RT "The alpha chain gene of H-2O has an unexpected location in the MHC.";  
RL J. Exp. Med. 176:477-483(1992).  
DR EMBL; M95514; AAB46387.1; -;  
DR HSSP; P01903; 1A6A.  
DR MGD; MGI:95924; H2-Oa.  
DR InterPro; IPR003597; Ig\_C1.  
SQ SEQUENCE 236 AA; 26205 MW; 9E1F01C034C90B20 CRC64;

Query Match 2.9%; Score 8; DB 7; Length 236;

Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 222 GLVGLLG 229  
Db 214 GLVGLLG 221

RESULT 14  
Q31359  
ID 031359 PRELIMINARY; PRT: 236 AA.  
AC 031359;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MHC CLASS II ALPHA CHAIN.  
OS Brachydanio rerio (zebrafish) (Zebra danio).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Ostariophysi;  
OC Cypriniformes; Cyprinidae; Danio.  
OX NCBI\_TaxID=7955;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=94011091; PubMed=8406613;  
RA Sultmann H., Mayer W.E., Figueroa F., O'Huigin C., Klein J.;  
RT "Zebrafish MHC class II alpha chain-encoding genes: polymorphism,  
RT expression, and function.";  
DE Immunogenetics 38:408-420(1993).  
GN H2-OA OR H-2OA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-B10.M; TISSUE=SPLEEN;  
RX MEDLINE=92364550; PubMed=1354242;  
RA Karlsson L., Peterson P.A.;  
RT "The alpha chain gene of H-2O has an unexpected location in the MHC.";  
RL J. Exp. Med. 176:477-483(1992).  
DR EMBL; M95514; AAB46387.1; -;  
DR HSSP; P01903; 1A6A.  
DR MGD; MGI:95924; H2-Oa.  
DR InterPro; IPR003597; Ig\_C1.  
SQ SEQUENCE 236 AA; 26136 MW; 3780A1609ACBE285 CRC64;

Query Match 2.9%; Score 8; DB 7; Length 236;  
Best Local Similarity 100.0%; Pred. No. 13;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 222 GLVGLLG 229  
Db 214 GLVGLLG 221

RESULT 15  
Q31150  
ID 031150 PRELIMINARY; PRT: 250 AA.  
AC 031150;  
DT 01-NOV-1996 (TREMBLrel. 01, Created)  
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE MHC CLASS II ALPHA CHAIN PRECURSOR.  
GN H2-OA OR H-2OA.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA STRAIN-B10.M; TISSUE=SPLEEN;  
RX MEDLINE=92364550; PubMed=1354242;  
RA Karlsson L., Peterson P.A.;  
RT "The alpha chain gene of H-2O has an unexpected location in the MHC.";  
RL J. Exp. Med. 176:477-483(1992).  
DR EMBL; M95514; AAB46387.1; -;  
DR HSSP; P01903; 1A6A.  
DR MGD; MGI:95924; H2-Oa.  
DR InterPro; IPR003597; Ig\_C1.

DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001003; MHC\_II\_alpha.  
 DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00993; MHC\_II\_alpha; 1.  
 DR SMART: SM00407; Igcl; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 KW Signal.  
 FT SIGNAL 1 25 POTENTIAL.  
 FT CHAIN 26 250 MHC CLASS II ALPHA CHAIN.  
 SQ SEQUENCE 250 AA; 28182 MW; C20A397B2EFA2004 CRC64;

Query Match 2.9%; Score 8; DB 7; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 GGLVGL 227  
 DB 222 GGLVGL 229

RESULT 16  
 O9QWV1 PRELIMINARY; PRT: 250 AA.  
 AC 01-MAY-2000 (TREMBLrel. 13, Created)  
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE H2-O ALPHA (HISTOCOMPATIBILITY 2, O REGION ALPHA LOCUS).  
 GN H2-OLPHA OR H2-OA.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_Taxid=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-129SVJ;  
 RA Rowen L., Qin S., Madan A., Loretz C., James R., Dors M., Mix L.,  
 RA Hall J., Lasky S., Hood L.;  
 RT "Sequence of the mouse major histocompatibility locus class II  
 RT region."  
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-C57BL/6J; TISSUE=URINARY BLADDER;  
 RX MEDLINE=21085660; PUBMED=11217851;  
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,  
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,  
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikolaio I., Pesole G., Quackenbush J.,  
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Balarelli R., Bersh G.,  
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Kombaerts P.,  
 RA Norone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyo-oka K., Wang K.H., Wertz C., Whitaker C., Wilming L.,  
 RA Wyshew-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kontsuki S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection."  
 RL Nature 409:685-690(2001).  
 DR EMBL: AF100956; AAC69906.1; -;  
 DR EMBL: AK020594; BAB32142.1; -;  
 DR HSRP: P01903; IAA6A.  
 DR MGD: MGI:95924; H2-Oa.  
 DR InterPro: IPR003597; Ig-cl.  
 DR InterPro: IPR003006; Ig\_MHC.  
 DR InterPro: IPR001003; MHC\_II\_alpha.

DR Pfam: PF00047; Ig\_1.  
 DR Pfam: PF00993; MHC\_II\_alpha; 1.  
 DR SMART: SM00407; Igcl; 1.  
 DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_1.  
 SQ SEQUENCE 250 AA; 28166 MW; 98BCF2F8926076A1 CRC64;

Query Match 2.9%; Score 8; DB 11; Length 250;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 220 GGLVGL 227  
 DB 222 GGLVGL 229

RESULT 17  
 O9X647 PRELIMINARY; PRT: 264 AA.  
 AC 09X647;  
 DT 01-NOV-1999 (TREMBLrel. 12, Created)  
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)  
 DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
 DE HYPOTHETICAL 28.2 KDA PROTEIN.  
 OS Aeromonas hydrophila.  
 OC Bacteria; Proteobacteria; gamma subdivision; Aeromonadaceae;  
 OC Aeromonas.  
 OX NCBI\_Taxid=644;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Aguilar A., Merino S., Noguera M.M., Regue M., Tomas J.M.;  
 RT "Two genes from the capsule of Aeromonas hydrophila (serogroup O:34)  
 RT confer serum resistance to Escherichia coli K-12 strains."  
 RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AF131869; AAD34732.1; -;  
 DR InterPro: IPR000326; PA\_PTPase.  
 DR Pfam: PF01569; PAP2; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 264 AA; 28163 MW; 8953984BCAC64FD6 CRC64;

Query Match 2.9%; Score 8; DB 2; Length 264;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 12 PCAALL 19  
 DB 18 PCAALL 25

RESULT 18  
 O9NPFO PRELIMINARY; PRT: 282 AA.  
 AC 09NPFO;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE 8D6 ANTIGEN (HYPOTHETICAL 29.0 KDA PROTEIN).  
 GN DKFZP564O1762.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Carim L., Estivill X., Escarceller M., Sumoy L.;  
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Aufray C., Ansoorge W., Ballabio A., Estivill X., Gibson K.,  
 RA Lehnach H., Poustka A., Lundeberg J.;  
 RT "The European IMAGE consortium for integrated Molecular analysis of  
 RT human gene transcripts.";



RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20193707; PubMed=10727470;  
RA Li L., Zhang X., Kovacic S., Long A.J., Bourque K., Wood C.R.,  
Choi Y.S.;  
RT "Identification of a human follicular dendritic cell molecule that  
stimulates germinal center B cell growth.";  
RL J. Exp. Med. 191:1077-1084(2000).  
RN [4]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN;  
RA Blum H., Baerends S., Mewes H.W., Gassenhuber J., Wiemann S.;  
RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.  
RN [5]  
RP SEQUENCE FROM N.A.  
RC TISSUE=KIDNEY ADENOCARCINOMA;  
RA Strausberg R.;  
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.  
RN [6]  
RP SEQUENCE FROM N.A.  
RC TISSUE=BRAIN, PRIMITIVE NEUROECTODERMAL;  
RA Strausberg R.;  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AL365455; CAB97010.1; -;  
DR EMBL; AF161254; AAF61850.1; -;  
DR EMBL; AL136652; CAB6587.1; -;  
DR EMBL; BC000668; AAH00668.1; -;  
DR EMBL; BC007083; AAH07083.1; -;  
DR HSSP; Q07954; JCR8.  
DR InterPro: IPR002172; LDL\_recept\_A.  
DR Pfam; PF000057; ldl\_recept\_a; 2.  
DR PRINTS; PR00261; LDLRECEPTOR.  
DR SMART; SM00192; LDla; 2.  
DR PROSITE; PS01209; LDLRA\_1; 2.  
DR PROSITE; PS50066; LDLRA\_2; 2.  
KW Glycoprotein.  
SQ SEQUENCE 282 AA; 28991 MW; 59E172986B220E4F CRC64;

Query Match 2.9%; Score 8; DB 4; Length 282;  
Best Local Similarity 100.0%; Pred. No. 15;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 16 LLLGLGL 23  
Db 22 LLLGLGL 29

RESULT 19  
O9FDT4  
ID O9FDT4 PRELIMINARY; PRT; 306 AA.  
AC O9FDT4;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)  
DE EXFOLIATIVE TOXIN A.  
GN SHETA.  
OS Staphylococcus hyicus.  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=1284;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=P-1;  
RX MEDLINE=20327593; PubMed=10869091;  
RA Watanabe T., Sato H., Hatakeyama Y., Matsuzawa T., Kawai M.,  
Aizawa C., Danbara H., Maehara N.;  
RT "Cloning of the gene coding for Staphylococcus hyicus exfoliative  
toxin A and its expression in Escherichia coli.";  
RL J. Bacteriol. 182:4101-4103(2000).  
DR EMBL; AB036768; BAB08178.1; -;  
SQ SEQUENCE 306 AA; 34379 MW; 60B7EDF3677ACDFF CRC64;

Query Match 2.9%; Score 8; DB 2; Length 306;  
Best Local Similarity 100.0%; Pred. No. 16;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 222 GLVGLGLG 229  
Db 12 GLVGLGLG 19

RESULT 20  
O99UT7  
ID O99UT7 PRELIMINARY; PRT; 315 AA.  
AC O99UT7;  
DT 01-JUN-2001 (TREMBlrel. 17, Created)  
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE HYPOTHETICAL PROTEIN SA1016 (HYPOTHETICAL PROTEIN SAV1173).  
GN SA1016 OR SAV1173.  
OS Staphylococcus aureus (strain N315), and  
Staphylococcus aureus (strain Mu50).  
OC Bacteria; Firmicutes; Bacillus/Clostridium group;  
OC Bacillus/Staphylococcus group; Staphylococcus.  
OX NCBI\_TaxID=158879, 158878;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC SPECIES=S. aureus (strain N315), and S. aureus (strain Mu50);  
RX MEDLINE=21311952; PubMed=11418146;  
RA Kuroda M., Ohta T., Uchihyama I., Baba T., Yuzawa H., Kobayashi I.,  
Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,  
Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,  
Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,  
Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,  
Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,  
Hattori M., Ogasawara N., Hayashi H., Hiratake K.;  
RT "Whole genome sequencing of methicillin-resistant Staphylococcus  
aureus.";  
RL Lancet 357:1225-1240(2001).  
DR EMBL; AP003132; BAB42268.1; -;  
DR EMBL; AP003361; BAB57335.1; -;  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 315 AA; 35236 MW; 74B814BDE7243139 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 315;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 222 GLVGLGLG 229  
Db 12 GLVGLGLG 19

RESULT 21  
O43324  
ID O43324 PRELIMINARY; PRT; 329 AA.  
AC O43324;  
DT 01-NOV-1996 (TREMBlrel. 01, Created)  
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)  
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)  
DE MAJOR STORAGE PROTEIN;  
OS Populus x canadensis.  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  
OC eudicots I; Malpighiales; Salicaceae; Populus.  
OX NCBI\_TaxID=3690;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92003681; PubMed=1912491;  
RA Clausen S., Apel K.;  
RT "Seasonal changes in the concentration of the major storage protein  
and its mRNA in xylem ray cells of poplar trees.";

Plant Mol. Biol. 17:669-678(1991).  
DR EMBL: S59422; AAB20113.2; -  
SQ SEQUENCE 329 AA; 36055 MW; 875C867A15042204 CRC64;

Query Match 2.9%; Score 8; DB 10; Length 329;  
Best Local Similarity 100.0%; Pred. No. 17;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21  
| | | | | | | |  
DB 7 AALLLGL 14

RESULT 22  
O93J03 PRELIMINARY; PRT; 432 AA.  
ID O93J03:  
AC O93J03:  
DT 01-DEC-2001 (TREMBLrel. 19, Created)  
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)  
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
DE PUTATIVE INTEGRAL MEMBRANE PROTEIN.  
GN SCBAC25F8.09.  
OS Streptomyces coelicolor.  
OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;  
OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=1902;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Seeger K., Harris D.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.  
RN [3]  
RP SEQUENCE FROM N.A.  
RC STRAIN-A3(2);  
RC MEDLINE=97000351; PubMed=8843436;  
RA Redenbach M., Kleser H.M., Denaplatte D., Elchner A., Cullum J.,  
RA Kinasch H., Hopwood D.A.;  
RT "A set of ordered cosmids and a detailed genetic and physical map for  
the 8 Mb Streptomyces coelicolor A3(2) chromosome.";  
RL Mol. Microbiol. 21:77-96(1996).  
DR EMBL: AL592126; CAC42144.1; -  
SQ SEQUENCE 432 AA; 43516 MW; DC222112875091B7 CRC64;

Query Match 2.9%; Score 8; DB 2; Length 432;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 16 LLLGLGL 23  
| | | | | | | |  
DB 70 LLLGLGL 77

RESULT 23  
O9HW78 PRELIMINARY; PRT; 443 AA.  
ID O9HW78:  
AC O9HW78:  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)  
DE HYPOTHEtical PROTEIN PA4323.  
GN PA4323.  
OS Pseudomonas aeruginosa.  
OC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;  
OC Pseudomonas.  
OX NCBI\_TaxID=287;  
RN [1]

RP SEQUENCE FROM N.A.  
RC STRAIN-ATCC 15692 / PA01;  
RX MEDLINE=20437337; PubMed=10984043;  
RA Stover C.K., Pham X.-Q.T., Ervin A.L., Mizoguchi S.D., Warrenner P.,  
RA Hickey M.J., Brinkman F.S.L., Huftagle W.O., Kowalik D.J., Lagrou M.,  
RA Gardner R.L., Goltry L., Tolentino E., Westbrook-Wedman S., Yuan Y.,  
RA Brody K.L., Coulter S.N., Folger K.R., Kas A., Lablitz K., Lim R.M.,  
RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,  
RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.;  
RT "Complete genome sequence of Pseudomonas aeruginosa PA01, an  
opportunistic pathogen.";  
RL Nature 406:959-964(2000).  
DR EMBL: AE004848; AAC07711.1; -  
DR InterPro: IPR002881; DUF58.  
DR InterPro: IPR002035; VFMA.  
DR Pfam: PF01882; DUF58; 1.  
DR SMART: SM00327; VMA; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 443 AA; 50359 MW; A3814456A5D5EBA8 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 443;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21  
| | | | | | | |  
DB 44 AALLLGL 51

RESULT 24  
O9CY76 PRELIMINARY; PRT; 473 AA.  
ID O9CY76:  
AC O9CY76:  
DT 01-JUN-2001 (TREMBLrel. 17, Created)  
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE 5730589L02RIK PROTEIN.  
GN 5730589L02RIK.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN-C57BL/6J; TISSUE=EMBRYO;  
RX MEDLINE=21085660; PubMed=11217851;  
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
RA Aizawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,  
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
RA Fleischmann W., Gaasterland T., Glass C., King B., Kochiya H.,  
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Queckenbush J.,  
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
RA Sakai K., Okido T., Furuno M., Aono H., Balderelli R., Barsh G.,  
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,  
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,  
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,  
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohlsuhl S.,  
RA Hayashizaki Y.;  
RT "Functional annotation of a full-length mouse cDNA collection.";  
RL Nature 409:685-690(2001).  
DR EMBL: AK019981; BAB31950.1; -  
DR MGD: MGI:1924832; 5730589L02RIK.  
SQ SEQUENCE 473 AA; 53504 MW; CE6F8E93C3D01C4F CRC64;

Query Match 2.9%; Score 8; DB 11; Length 473;

Best Local Similarity 100.0%; Pred. No. 24;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 219 LGIGLVIG 226  
Db 441 LGIGLVIG 448

RESULT 25

ID 005295 PRELIMINARY; PRT; 473 AA.

AC 005295; (TREMblrel. 04, Created)

DT 01-JUL-1997 (TREMblrel. 04, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE HYPOHETICAL 49.5 KDA PROTEIN.

GN PADD36 OR RV1193 OR MTC1364.05.

OS Mycobacterium tuberculosis.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1773;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=H37RV; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,

RA Gordon S.V., Eiglmeler K., Gas S., Barry C.E. III, Tekala F.,

RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,

RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,

RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,

RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,

RA Salston J.E., Taylor K., Whitehead S., Barrell B.G.;

RT "Deciphering the biology of Mycobacterium tuberculosis from the

RT complete genome sequence."

RL Nature 393:537-544(1998).

DR EMBL: Z93777; CAB07836.1; -.

DR HSSP: P08659; ILCI.

DR Tuberculist: RV1193; -.

DR InterPro: IPR000873; AMP-bind.

DR InterPro: IPR003015; HLH\_Myc.

DR Pfam: PF00501; AMP-binding; 1.

DR PRINTS: PR00154; AMPBINDING.

DR PROSITE: PS00455; AMP\_BINDING; 1.

DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.

KW Hypothetical protein: Complete proteome.

SEQ SEQUENCE 473 AA; 49520 MW; 39ECC2BD0D2BAD3D CRC64;

Query Match 2.9%; Score 8; DB 16; Length 473;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVIGLIG 229  
Db 184 GLVIGLIG 191

RESULT 26

ID 050017 PRELIMINARY; PRT; 476 AA.

AC 050017; (TREMblrel. 01, Created)

DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE XCLC (ACTV-COA SYNTHASE).

GN XCLC OR ML1051.

OS Mycobacterium leprae.

OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;

OC Actinomycetales; Corynebacterineae; Mycobacteriaceae; Mycobacterium.

OX NCBI\_TaxID=1769;

RN [1]

RP SEQUENCE FROM N.A.

RA Smith D.R., Robison K.;

RL Submitted (APR-1995) to the EMBL/GenBank/DBJ databases.

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=TN;

RA MEDLINE=21128732; PubMed=11234002;

RA Cole S.T., Eiglmeler K., Parkhill J., James K.D., Thomson N.R.,

RA Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,

RA Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,

RA Davies R.M., Devlin K., Duthoy S., Felwell T., Fraser A., Hamlin N.,

RA Holroyd S., Hornsby T., Jagels K., Lacroix C., McLean J., Moule S.,

RA Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,

RA Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,

RA Barrell B.G.;

RT "Massive gene decay in the leprosy bacillus."

RL Nature 408:1007-1011(2001).

DR EMBL: U15181; AAA62961.1; -.

DR HSSP: AL583920; CAC1432.1; -.

DR Leprona: ML1051; -.

DR InterPro: IPR000873; AMP-bind.

DR InterPro: IPR003015; HLH\_Myc.

DR Pfam: PF00501; AMP-binding; 1.

DR PRINTS: PR00154; AMPBINDING.

DR PROSITE: PS00455; AMP\_BINDING; 1.

DR PROSITE: PS00038; HELIX\_LOOP\_HELIX; UNKNOWN\_1.

KW Complete proteome.

SEQ SEQUENCE 476 AA; 50130 MW; 4F8DEED72059E66E CRC64;

Query Match 2.9%; Score 8; DB 16; Length 476;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 222 GLVIGLIG 229  
Db 187 GLVIGLIG 194

RESULT 27

ID 097097 PRELIMINARY; PRT; 513 AA.

AC 097097; (TREMblrel. 18, Created)

DT 01-OCT-2001 (TREMblrel. 18, Last sequence update)

DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)

DE SODIUM:SOLUTE SYMPORTER FAMILY PROTEIN.

GN SPI328.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;

OC Streptococcus.

OX NCBI\_TaxID=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TIGR4;

RA MEDLINE=21357209; PubMed=11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

RA Holtzaple E., Khouri H., Wolf A.M., Uterback T.R., Hansen C.L.,

RA McDonald L.A., Feldblyum T.V., Angiolli S., Dickinson T., Hickey E.K.,

RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

RT "Complete genome sequence of a virulent isolate of Streptococcus

RT pneumoniae."

RL Science 293:498-506(2001).

DR EMBL: AE007431; AAK75426.1; -.

DR TIGR: SPI328; -.

DR InterPro: IPR001734; Na\_solut\_sympor.

DR Pfam: PF00474; SSF; 1.

DR PROSITE: PS00456; NA\_solut\_symp\_1; UNKNOWN\_1.

DR PROSITE: PS50283; NA\_SOLUT\_SYMP\_3; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 513 AA; 55768 MW; D9E9CE6A9A8417E7 CRC64;

Query Match 2.9%; Score 8; DB 16; Length 513;  
 Best Local Similarity 100.0%; Pred. No. 25;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 222 GLVLGLG 229  
 |||||  
 DB 414 GLVLGLG 421

RESULT 28

ID 09JLT2 PRELIMINARY; PRT; 576 AA.  
 AC 09JLT2:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE TRHHLASE (EC 3.2.1.28) (2210412M19RIK PROTEIN).  
 GN TRH OR 2210412M19RIK.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-DDY; TISSUE=INTESTINAL MUCOSA;  
 RA Ohla T., Kudo N., Ariyasu H., Yanai Y., Takeuchi M., Ikegami H.,  
 RA Kurimoto M.;  
 RL Submitted (MAR-1999) to the EMBL/GenBank/DBJ databases.

RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J; TISSUE=STOMACH;  
 RA MEDLINE=21085660; PubMed=11217851;  
 RA Kawai J., Shnagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,  
 RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,  
 RA Aitawa K., Itawa M., Nishi K., Kiyosawa H., Kondo S., Yamana I.,  
 RA Saito T., Okazaki Y., Gojohori T., Bono H., Kasukawa T., Saito R.,  
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,  
 RA Flieschmann W., Gaasterland T., Gissi C., King B., Kochia H.,  
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Peesle G., Quackenbush J.,  
 RA Schirml L.M., Steubli F., Suzuki R., Tomita M., Wagner L., Washio T.,  
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,  
 RA Blake J., Botfield D., Bojunga N., Carninci P., de Bonaldo M.F.,  
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,  
 RA Guellinich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,  
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,  
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,  
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,  
 RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilting L.,  
 RA Wyszynski-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohlski S.,  
 RA Hayashizaki Y.;  
 RT "Functional annotation of a full-length mouse cDNA collection.";  
 RL Nature 409:685-690(2001).  
 DR EMBL; AF136944; AA61430.1; -  
 DR EMBL; AK008912; BAB25963.1; -  
 DR MGI; MGI:1926230; Treh.  
 DR InterPro: IPR001661; Trehalase.  
 DR Pfam; PF01204; Trehalase; 1.  
 DR PRINTS; PR00744; GLHYDRLASE37.  
 DR PROSITE; PS00927; TREHALASE\_1; 1.  
 DR PROSITE; PS00928; TREHALASE\_2; 1.  
 KW Hydrolase; Glycosidase.  
 SQ SEQUENCE 576 AA; 65401 MW; 53CDA6A10511520E CRC64;

Query Match 2.9%; Score 8; DB 11; Length 576;  
 Best Local Similarity 100.0%; Pred. No. 28;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLGLGL 23  
 |||||  
 DB 8 LLLGLGL 15

RESULT 29

ID 09P264 PRELIMINARY; PRT; 621 AA.  
 AC 09P264:  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE KIA1464 PROTEIN (FRAGMENT).  
 GN KIA1464.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=20277482; PubMed=10819331;  
 RA Nagase T., Kikuno R., Ishikawa K., Hirose M., Ohara O.;  
 RT Prediction of the coding sequences of unidentified human  
 genes. XVII. The complete sequences of 100 new cDNA clones from brain  
 which code for large proteins in vitro.";  
 RL DNA Res. 7:143-150(2000).  
 DR EMBL; AB040897; BAA95988.1; -

DR InterPro: IPR003877; SPRY.  
 DR InterPro: IPR003878; SPRY\_domain.  
 DR Pfam; PF00622; SPRY; 1.  
 DR SMART; SM00449; SPRY; 1.  
 FT NON\_TER  
 SQ SEQUENCE 621 AA; 67385 MW; DBC285CDB9CFD40C CRC64;

Query Match 2.9%; Score 8; DB 4; Length 621;  
 Best Local Similarity 100.0%; Pred. No. 30;  
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 261 TPIOEQA 268  
 |||||  
 DB 284 TPIOEQA 291

RESULT 30

ID 060279 PRELIMINARY; PRT; 768 AA.  
 AC 060279:  
 DT 01-AUG-1998 (TREMBLrel. 07, Created)  
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)  
 DE KIA0527 PROTEIN (FRAGMENT).  
 GN KIA0527.  
 OS Homo sapiens (Human).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;

RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=BRIN;  
 RA MEDLINE=98290545; PubMed=9628581;  
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,  
 RA Ohara O.;  
 RT Prediction of the coding sequences of unidentified human genes. IX.  
 RT The complete sequences of 100 new cDNA clones from brain which can  
 code for large proteins in vitro.";  
 RL DNA Res. 5:31-39(1998).  
 DR EMBL; AB011099; BAA25453.1; -

DR InterPro: IPR000538; Link.  
 DR InterPro: IPR000436; Sush1\_SCR\_CCP.  
 DR Pfam; PF00084; sush1; 1.  
 DR SMART; SM00032; CCP; 1.  
 DR SMART; SM00445; Link; 1.

FT NON\_TER 1 1  
SQ SEQUENCE 768 AA; 82680 MM; B97A932B44883536 CRC64;

Query Match 2.9%; Score 8; DB 4; Length 768;  
Best Local Similarity 100.0%; Pred. NO. 36;  
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLGL 21  
| | | | | | | |  
Db 161 AALLLGL 168

Search completed: June 18, 2002, 14:33:01  
Job time: 214 sec

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GenCore version 4.5  
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## OM protein - protein search, using sw model

Run on: June 18, 2002, 14:25:22 ; Search time 13.13 Seconds  
(without alignments)  
515.300 Million cell updates/sec

Title: US-09-852-845-2

Perfect score: 277

Sequence: 1 MCVGARRLGRGPCALLLLG.....SFRPIQEQADAHSTLAKI 277

## Scoring table:

OLIGO  
Gapop 60.0 , Gapext 60.0

Searched: 231628 seqs, 24425594 residues

Word size: 0

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 50 summaries

## Database :

Issued\_Patents\_AA:\*

- 1: /cgn2\_6/ptodata/2/1aa/5A\_COMB.pep.\*
- 2: /cgn2\_6/ptodata/2/1aa/5B\_COMB.pep.\*
- 3: /cgn2\_6/ptodata/2/1aa/6A\_COMB.pep.\*
- 4: /cgn2\_6/ptodata/2/1aa/6B\_COMB.pep.\*
- 5: /cgn2\_6/ptodata/2/1aa/PCUS\_COMB.pep.\*
- 6: /cgn2\_6/ptodata/2/1aa/backfilltest.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result	Query	Match	Length	DB	ID	Description
No.	Score					
1	277	100.0	277	2	US-08-147-784-2	Sequence 2, Appli
2	277	100.0	277	4	US-08-195-967-2	Sequence 2, Appli
3	277	100.0	277	4	US-09-006-353A-12	Sequence 12, Appli
4	277	100.0	277	4	US-08-472-940-2	Sequence 2, Appli
5	56	20.2	56	4	US-08-866-545-10	Sequence 10, Appli
6	12	4.3	41	1	US-08-050-319B-44	Sequence 44, Appli
7	12	4.3	41	2	US-08-465-982-44	Sequence 44, Appli
8	12	4.3	133	4	US-08-468-560C-8	Sequence 8, Appli
9	12	4.3	139	2	US-08-219-237B-8	Sequence 8, Appli
10	12	4.3	140	4	US-08-477-347-17	Sequence 17, Appli
11	12	4.3	140	8	US-08-476-862-8	Sequence 8, Appli
12	12	4.3	205	3	US-08-974-022-51	Sequence 51, Appli
13	12	4.3	205	4	US-08-795-445A-51	Sequence 51, Appli
14	12	4.3	205	4	US-08-795-447A-51	Sequence 51, Appli
15	12	4.3	205	4	US-08-974-186-51	Sequence 51, Appli
16	12	4.3	206	1	US-08-795-446B-51	Sequence 51, Appli
17	12	4.3	206	1	US-08-097-827-7	Sequence 7, Appli
18	12	4.3	206	1	US-08-494-574-7	Sequence 7, Appli
19	12	4.3	438	1	US-08-097-827-11	Sequence 11, Appli
20	12	4.3	438	1	US-08-494-574-11	Sequence 11, Appli
21	9	3.2	625	3	US-08-996-139-15	Sequence 15, Appli
22	9	3.2	625	3	US-08-995-659-15	Sequence 15, Appli
23	9	3.2	625	4	US-09-215-649A-15	Sequence 15, Appli
24	7	2.5	30	4	US-09-105-390-20	Sequence 20, Appli
25	7	2.5	105	4	US-09-124-671-17	Sequence 17, Appli
26	7	2.5	109	4	US-09-124-671-19	Sequence 19, Appli
27	7	2.5	109	4	US-09-124-671-21	Sequence 21, Appli

28	7	2.5	115	4	US-09-124-671-13	Sequence 13, Appli
29	7	2.5	115	4	US-09-124-671-15	Sequence 15, Appli
30	7	2.5	128	1	US-08-478-039-110	Sequence 110, App
31	7	2.5	128	1	US-08-476-349A-110	Sequence 110, App
32	7	2.5	128	4	US-08-523-894-4	Sequence 4, Appli
33	7	2.5	134	4	US-09-124-671-34	Sequence 34, Appli
34	7	2.5	144	2	US-08-341-843B-39	Sequence 39, Appli
35	7	2.5	144	2	US-08-427-497E-44	Sequence 44, Appli
36	7	2.5	209	2	US-08-827-279-1	Sequence 1, Appli
37	7	2.5	233	4	US-08-523-894-6	Sequence 6, Appli
38	7	2.5	243	4	US-09-188-930-295	Sequence 295, App
39	7	2.5	261	2	US-08-484-905-111	Sequence 111, App
40	7	2.5	261	3	US-08-481-985B-111	Sequence 111, App
41	7	2.5	261	4	US-08-370-476-111	Sequence 12, Appli
42	7	2.5	327	1	US-08-375-962B-12	Sequence 12, Appli
43	7	2.5	327	2	US-08-562-114B-12	Sequence 12, Appli
44	7	2.5	327	4	US-08-729-594A-12	Sequence 12, Appli
45	7	2.5	335	2	US-08-875-062-3	Sequence 3, Appli
46	7	2.5	336	4	US-09-105-390-52	Sequence 52, Appli
47	7	2.5	406	4	US-08-506-296B-5	Sequence 5, Appli
48	7	2.5	415	1	US-08-110-286A-2	Sequence 2, Appli
49	7	2.5	415	1	US-08-110-286A-6	Sequence 6, Appli
50	7	2.5	415	4	US-08-981-109B-10	Sequence 10, Appli

## ALIGNMENTS

RESULT 1  
US-08-147-784-2  
; Sequence 2, Application US/08147784  
; Patent No. 5821332  
; GENERAL INFORMATION:  
; APPLICANT: Godfrey, Wayne  
; APPLICANT: Buck, David  
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourile and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/147,784  
; FILING DATE: 03-NOV-1993  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 05490A-220  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO. 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-147-784-2  
Query Match 100.0%; Score 277; DB 2; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1,4e-260;

Matches 277: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60  
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120  
Db 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120

Qy 121 PGVDCAPCPGHPSPGDNACRPMCTCTAGKHTTLOPASNSSDAICEDRDPPTQOETQ 180  
Db 121 PGVDCAPCPGHPSPGDNACRPMCTCTAGKHTTLOPASNSSDAICEDRDPPTQOETQ 180

Qy 181 GPPARITVQPTWAMPRTSGSPSTREVEYVGGRAVAAILGLGLVGLLPLAILLALYLL 240  
Db 181 GPPARITVQPTWAMPRTSGSPSTREVEYVGGRAVAAILGLGLVGLLPLAILLALYLL 240

Qy 241 RRDQRLPPDAHKPPGGGSRFTPIQEBQADAHSTLAKI 277  
Db 241 RRDQRLPPDAHKPPGGGSRFTPIQEBQADAHSTLAKI 277

RESULT 2  
US-08-195-967-2  
; Sequence 2, Application US/08195967  
; Patent No. 6242566  
; GENERAL INFORMATION:  
; APPLICANT: Godfrey, Wayne  
; APPLICANT: Engleman, Edgar G.  
; TITLE OF INVENTION: LIGAND (ACT-4-L) TO A RECEPTOR ON THE SURFACE OF ACTIVATED  
; TITLE OF INVENTION: CD4+ T-CELLS  
; NUMBER OF SEQUENCES: 4  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Kourile and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/195,967  
; FILING DATE: 10-FEB-1994  
; CLASSIFICATION: 424  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M  
; REGISTRATION NUMBER: 30,223  
; REFERENCE/DOCKET NUMBER: 05490A-230  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-195-967-2

Query Match 100.0%; Score 277; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1,4e-260; Mismatches 0; Indels 0; Gaps 0;

Matches 277: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60  
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120  
Db 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120

Qy 121 PGVDCAPCPGHPSPGDNACRPMCTCTAGKHTTLOPASNSSDAICEDRDPPTQOETQ 180  
Db 121 PGVDCAPCPGHPSPGDNACRPMCTCTAGKHTTLOPASNSSDAICEDRDPPTQOETQ 180

Qy 181 GPPARITVQPTWAMPRTSGSPSTREVEYVGGRAVAAILGLGLVGLLPLAILLALYLL 240  
Db 181 GPPARITVQPTWAMPRTSGSPSTREVEYVGGRAVAAILGLGLVGLLPLAILLALYLL 240

Qy 241 RRDQRLPPDAHKPPGGGSRFTPIQEBQADAHSTLAKI 277  
Db 241 RRDQRLPPDAHKPPGGGSRFTPIQEBQADAHSTLAKI 277

RESULT 3  
US-09-006-353A-12  
; Sequence 12, Application US/09006353A  
; Patent No. 6261801  
; GENERAL INFORMATION:  
; APPLICANT: WEI, YING-FEI  
; APPLICANT: YU, GUO-LIANG  
; APPLICANT: GENTZ, REINER  
; APPLICANT: RUBEN, STEVEN  
; TITLE OF INVENTION: TUMOR NECROSIS FACTOR RECEPTOR 5  
; NUMBER OF SEQUENCES: 26  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.  
; STREET: 9410 KEY WEST AVENUE  
; CITY: ROCKVILLE  
; STATE: MD  
; COUNTRY: US  
; ZIP: 20850  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: IBM PC compatible  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/006,353A  
; FILING DATE:  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: BROOKES, ANDERS A  
; REGISTRATION NUMBER: 36,373  
; REFERENCE/DOCKET NUMBER: PF341  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (301) 309-8504  
; TELEFAX: (301) 309-8512  
; INFORMATION FOR SEQ ID NO: 12:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-006-353A-12

Query Match 100.0%; Score 277; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1,4e-260; Mismatches 0; Indels 0; Gaps 0;

Matches 277: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60  
Db 1 MCVGARRLGRPCALLLLGLSTVTLGHCVGDTYPSNDRCHCRPGNGMVSRCRSQ 60

Qy 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120  
Db 61 NTVCRCPCGGFNDVYSSPKCKPCTWCNLRSGSERKQLCTATODTVCRCRAGTQPLDSYK 120



Qy 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQPA NSSDAICEDRDPATOPQETQ 180  
Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQPA NSSDAICEDRDPATOPQETQ 180  
Qy 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGVLGILGPIALILATLYLL 240  
Db 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGVLGILGPIALILATLYLL 240  
Qy 241 RRDORLPPDAHKPPGGGSRFPTRIOEQADAHSTLAKI 277  
Db 241 RRDORLPPDAHKPPGGGSRFPTRIOEQADAHSTLAKI 277

## RESULT 4

US-08-472-940-2  
; Sequence 2, Application US/08472940  
; Patent No. 6277962  
; GENERAL INFORMATION:  
; APPLICANT: Godfrey, Wayne  
; APPLICANT: Buck, David  
; APPLICANT: Engleman, Edgar G.  
; TITLE OF INVENTION: RECEPTOR ON THE SURFACE OF ACTIVATED  
; TITLE OF INVENTION: CD4+ T-CELLS: ACT-4  
; NUMBER OF SEQUENCES: 2  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Townsend and Townsend Khourie and Crew  
; STREET: 379 Lytton Avenue  
; CITY: Palo Alto  
; STATE: California  
; COUNTRY: US  
; ZIP: 94301  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/472,940  
; FILING DATE: 06-JUN-1995  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/147,784  
; FILING DATE: 03-NOV-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Smith, William M.  
; REGISTRATION NUMBER: 30,223  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 326-2400  
; TELEFAX: (415) 326-2422  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 277 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-472-940-2

Query Match 100.0%; Score 277; DB 4; Length 277;  
Best Local Similarity 100.0%; Pred. No. 1.4e-260;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MCVGARRIRGRPCALLLIGLSTVYTGHCYGDYPPSNDRCCHCRGNGVSRCSRSQ 60  
Db 1 MCVGARRIRGRPCALLLIGLSTVYTGHCYGDYPPSNDRCCHCRGNGVSRCSRSQ 60  
Qy 61 NTVCAPCGPGFYNDVSSKPKCKPTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSYK 120  
Db 61 NTVCAPCGPGFYNDVSSKPKCKPTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSYK 120  
Qy 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQPA NSSDAICEDRDPATOPQETQ 180  
Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQPA NSSDAICEDRDPATOPQETQ 180

Db 121 PGVDCAPCPGHFSPGDNQACKPMTNCTLAGKHTLQPA NSSDAICEDRDPATOPQETQ 180  
Qy 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGVLGILGPIALILATLYLL 240  
Db 181 GPPARPITVQTEAMPRTSOGSPSTRPVPGRAVAAILGVLGILGPIALILATLYLL 240  
Qy 241 RRDORLPPDAHKPPGGGSRFPTRIOEQADAHSTLAKI 277  
Db 241 RRDORLPPDAHKPPGGGSRFPTRIOEQADAHSTLAKI 277

## RESULT 5

US-08-866-545-10  
; Sequence 10, Application US/08866545  
; Patent No. 6265535  
; GENERAL INFORMATION:  
; APPLICANT: Greene, Mark I.  
; APPLICANT: Murali, Ramachandran  
; APPLICANT: Takasaki, Wataru  
; TITLE OF INVENTION: PEPTIDES AND PEPTIDE  
; TITLE OF INVENTION: ANALOGUES DESIGNED FROM BINDING SITES OF TUMOR  
; TITLE OF INVENTION: NECROSIS FACTOR RECEPTOR SUPERFAMILY AND THEIR  
; NUMBER OF SEQUENCES: 27  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Pennie & Edmonds LLP  
; STREET: 1155 Avenue of the Americas  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10036-2811  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FASTSEQ Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/866,545  
; FILING DATE: 30-MAY-1997  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER:  
; FILING DATE:  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Coruzzi, Laura A.  
; REGISTRATION NUMBER: 30,742  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 650-493-4935  
; TELEFAX: 650-493-5556  
; TELEX: 66141 PENNIE  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 56 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: No. 6265535e  
; US-08-866-545-10

Query Match 20.2%; Score 56; DB 4; Length 56;  
Best Local Similarity 100.0%; Pred. No. 4.1e-47;  
Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 64 CRPCGGPGFYNDVSSKPKCKPTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSY 119  
Db 1 CRPCGGPGFYNDVSSKPKCKPTWCNLRSGSERKQICTATQDVTVCRCRACGTQPLDSY 119

## RESULT 6

US-08-050-319B-44  
; Sequence 44, Application US/08050319B

Patent No. 5633145  
GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robblins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319B  
FILING DATE: 10-May-1993  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Robblins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-050-319B-44

Query Match 4.3%; Score 12; DB 1; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
Db 12 NOACKPWTNCTL 23

RESULT 7  
US-08-465-982-44  
Sequence 44, Application US/08465982  
Patent No. 5863786  
GENERAL INFORMATION:  
APPLICANT: M.Feldmann, P.W. Gray,  
APPLICANT: M.J.C. Turner, F.M Brennan  
TITLE OF INVENTION: Modified human TNFalpha (Tumor  
TITLE OF INVENTION: Necrosis Factor alpha) Receptor  
NUMBER OF SEQUENCES: 57  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Reed & Robblins  
STREET: 635 Bryant Street  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94301  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/465,982

FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/050,319  
FILING DATE: 10-May-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Robblins, Roberta L.  
REGISTRATION NUMBER: 33,208  
REFERENCE/DOCKET NUMBER: 5150-0030  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 617-8999  
TELEFAX: (415) 327-3231  
INFORMATION FOR SEQ ID NO: 44:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 41 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-465-982-44

Query Match 4.3%; Score 12; DB 2; Length 41;  
Best Local Similarity 100.0%; Pred. No. 0.00013;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
Db 12 NOACKPWTNCTL 23

RESULT 8  
US-08-468-560C-8  
Sequence 8, Application US/08468560C  
Patent No. 6270998  
GENERAL INFORMATION:  
APPLICANT: NAGATA, Shigekazu  
APPLICANT: ITOH, Naoto  
APPLICANT: YONEHARA, Shin  
TITLE OF INVENTION: DNA CODING FOR HUMAN CELL SURFACE  
TITLE OF INVENTION: ANTIGEN  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: BIRCH, STEWART, KOLASCH & BIRCH, LLP.  
STREET: P.O. BOX 747  
CITY: FALLS CHURCH  
STATE: VA  
COUNTRY: USA  
ZIP: 22040-0747  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/468,560C  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: MURPHY JR., GERLAD M.  
REGISTRATION NUMBER: 28,977  
REFERENCE/DOCKET NUMBER: 20-4393P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 703-205-8000  
TELEFAX: 703-205-8050  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 133 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-468-560C-8

Query Match 4.3%; Score 12; DB 4; Length 133;  
Best Local Similarity 100.0%; Pred. No. 0.00039;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
DB 104 NOACKPWTNCTL 115

RESULT 9  
US-08-219-237B-8  
; Sequence 8, Application US/08219237B  
; Patent No. 5874546  
; GENERAL INFORMATION:  
; APPLICANT: NAGATA, Shigekazu  
; APPLICANT: ITOH, Naoto  
; APPLICANT: YONEHARA, Shin  
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen  
; NUMBER OF SEQUENCES: 11  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: James W. Hellwege  
; STREET: P.O. Box 2266 Eads Station  
; CITY: Arlington  
; STATE: Virginia  
; COUNTRY: USA  
; ZIP: 22202  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/219,237B  
; FILING DATE: 28-MAR-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/872,129  
; FILING DATE: 22-APR-1992  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: James W. Hellwege  
; REGISTRATION NUMBER: 28,808  
; REFERENCE/DOCKET NUMBER: 516762  
; INFORMATION FOR SEQ ID NO: 8:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 139 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; US-08-219-237B-8

Query Match 4.3%; Score 12; DB 2; Length 139;  
Best Local Similarity 100.0%; Pred. No. 0.0004;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
DB 110 NOACKPWTNCTL 121

RESULT 10  
US-08-477-347-17  
; Sequence 17, Application US/08477347  
; Patent No. 6232446  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; TITLE OF INVENTION: TNF LIGANDS

; NUMBER OF SEQUENCES: 17  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NETMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/477,347  
; FILING DATE:  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/115,685  
; FILING DATE:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: IL 106271  
; FILING DATE: 08-JUL-1993  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Townsend, G. Kevin  
; REGISTRATION NUMBER: 34,033  
; REFERENCE/DOCKET NUMBER: WALLACH=10  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202-628-5197  
; TELEFAX: 202-737-3528  
; TELEX: 248633  
; INFORMATION FOR SEQ ID NO: 17:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 140 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: peptide  
; US-08-477-347-17

Query Match 4.3%; Score 12; DB 4; Length 140;  
Best Local Similarity 100.0%; Pred. No. 0.00041;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149  
DB 111 NOACKPWTNCTL 122

RESULT 11  
US-08-476-862-8  
; Sequence 8, Application US/08476862  
; Patent No. 6262239  
; GENERAL INFORMATION:  
; APPLICANT: WALLACH, David  
; APPLICANT: BIGDA, Jacek  
; APPLICANT: BELETSKY, Igor  
; APPLICANT: METT, Igor  
; APPLICANT: ENGELMANN, Hartmut  
; TITLE OF INVENTION: TNF INHIBITORS  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BROWDY AND NETMARK  
; STREET: 419 Seventh Street, N.W.  
; CITY: Washington  
; STATE: D.C.  
; COUNTRY: USA  
; ZIP: 20004  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS

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SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,862
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 107267
FILING DATE: 12-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 94039
FILING DATE: 06-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 91229
FILING DATE: 06-AUG-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 90339
FILING DATE: 18-MAY-1989
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, ROGER L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: WALLACH-12A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 140 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-476-862-8

Query Match
Best Local Similarity 100.0%; Score 12; DB 4; Length 140;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWTNCTL 149
DB 111 NOACKPWTNCTL 122

RESULT 12
US-08-974-022-51
Sequence 51, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
```

```
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-51
```

```
Query Match
Best Local Similarity 100.0%; Score 12; DB 3; Length 205;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
QY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146
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```
RESULT 13
US-08-795-445A-51
Sequence 51, Application US/08795445A
Patent No. 6284485
```

```
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,445A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 205 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-445A-51
```

```
Query Match
Best Local Similarity 100.0%; Score 12; DB 4; Length 205;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 138 NOACKPWTNCTL 149
DB 135 NOACKPWTNCTL 146
```

RESULT 14  
US-08-795-447A-51  
Sequence 51, Application US/08795447A  
Patent No. 6284728  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: Osteoprotegerin  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: One Amgen Center Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91362-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,447A  
FILING DATE:  
CLASSIFICATION: 51A  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378D2  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-447A-51

Query Match 4.3%; Score 12; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149  
DB 135 NOACKPWTNCTL 146

RESULT 15  
US-08-974-186-51  
Sequence 51, Application US/08974186  
Patent No. 6284740  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/974,186  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-974-186-51

Query Match 4.3%; Score 12; DB 4; Length 205;  
Best Local Similarity 100.0%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149  
DB 135 NOACKPWTNCTL 146

RESULT 16  
US-08-795-446B-51  
Sequence 51, Application US/08795446B  
Patent No. 6288032  
GENERAL INFORMATION:  
APPLICANT: Boyle, William J.  
APPLICANT: Lacey, David L.  
APPLICANT: Calzone, Frank J.  
APPLICANT: Chang, Ming-Shi  
TITLE OF INVENTION: OSTEOPROTEGERIN  
NUMBER OF SEQUENCES: 53  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Amgen Inc.  
STREET: 1840 Dehavilland Drive  
CITY: Thousand Oaks  
STATE: California  
COUNTRY: USA  
ZIP: 91320-1789  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/795,446B  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/577,788  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Winter, Robert B.  
REFERENCE/DOCKET NUMBER: A-378  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 205 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-795-446B-51

Query Match 4.3%; Score 12; DB 4; Length 205;

Best Local Similarity 100.0%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 138 NOACKPWNTCTL 149  
DB 135 NOACKPWNTCTL 146

## RESULT 17

US-08-097-827-7  
Sequence 7, Application US/08097827

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: Novel cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-Jul-1993

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0730

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE DESCRIPTION: SEQ ID NO: 7:

US-08-097-827-7

Query Match 4.3%; Score 12; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWNTCTL 149

DB 136 NOACKPWNTCTL 147

## RESULT 18

US-08-494-574-7

Sequence 7, Application US/08494574

Patent No. 5783665

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: No. 5783665el cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/494,574

FILING DATE: 22-JUN-1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-Jul-1993

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:

TELEPHONE: 206-587-0730

INFORMATION FOR SEQ ID NO: 7:

SEQUENCE CHARACTERISTICS:

LENGTH: 206 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-494-574-7

Query Match 4.3%; Score 12; DB 1; Length 206;  
Best Local Similarity 100.0%; Pred. No. 0.00058;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 NOACKPWNTCTL 149

DB 136 NOACKPWNTCTL 147

## RESULT 19

US-08-097-827-11

Sequence 11, Application US/08097827

GENERAL INFORMATION:

APPLICANT: Baum, Peter

Goodwin, Ray

Fanslow, William

Gayle, Richard

TITLE OF INVENTION: Novel cytokine which is a ligand for

OX40

NUMBER OF SEQUENCES: 13

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunex Corporation

STREET: 51 University Street

CITY: Seattle

STATE: WA

COUNTRY: USA

ZIP: 98101

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/097,827

FILING DATE: 23-Jul-1993

CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.

REGISTRATION NUMBER: 34,693

REFERENCE/DOCKET NUMBER: 2806

TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
SEQUENCE DESCRIPTION: SEQ ID NO: 11:  
US-08-097-827-11

Query Match 4.3%; Score 12; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWNTCTL 149  
|||||  
DB 136 NOACKPWNTCTL 147

RESULT 20  
US-08-494-574-11  
Sequence 11, Application US/08494574  
Patent No. 5783665  
GENERAL INFORMATION:  
APPLICANT: Baum, Peter  
APPLICANT: Goodwin, Ray  
APPLICANT: Fanslow, William  
APPLICANT: Gayle, Richard  
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for  
TITLE OF INVENTION: 0X40  
NUMBER OF SEQUENCES: 13  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/494,574  
FILING DATE: 22-JUN-1995  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/097,827  
FILING DATE: 23-JUL-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia A.  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2806  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-587-0730  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 438 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-494-574-11

Query Match 4.3%; Score 12; DB 1; Length 438;  
Best Local Similarity 100.0%; Pred. No. 0.0012;  
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 138 NOACKPWNTCTL 149  
|||||

DB 136 NOACKPWNTCTL 147

RESULT 21  
US-08-996-139-15  
Sequence 15, Application US/08996139  
Patent No. 6017729  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
APPLICANT: Galibert, Laurent  
APPLICANT: Maraskovsky, Eugene  
TITLE OF INVENTION: Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: Apple Power Macintosh  
OPERATING SYSTEM: Apple Operating System 7.5.5  
SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/996,139  
FILING DATE: 22 DECEMBER 1997  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 60/064,671  
FILING DATE: 14 OCTOBER 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/813,509  
FILING DATE: 07 MARCH 1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: USSN 08/772,330  
FILING DATE: 23 DECEMBER 1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Perkins, Patricia Anne  
REGISTRATION NUMBER: 34,693  
REFERENCE/DOCKET NUMBER: 2851-A  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (206)587-0430  
TELEFAX: (206)233-0644  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 625 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-996-139-15

Query Match 3.2%; Score 9; DB 3; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWNTCTL 149  
|||||  
DB 170 CKPWNTCTL 178

RESULT 22  
US-08-995-659-15  
Sequence 15, Application US/08995659  
Patent No. 6242213  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
APPLICANT: Galibert, Laurent  
APPLICANT: Maraskovsky, Eugene  
TITLE OF INVENTION: Ligand for Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19

;; CORRESPONDENCE ADDRESS:  
;; ADDRESSEE: Immunex Corporation, Law Department  
;; STREET: 51 University Street  
;; CITY: Seattle  
;; STATE: WA  
;; COUNTRY: USA  
;; ZIP: 98101  
;;  
;; COMPUTER READABLE FORM:  
;; MEDIUM TYPE: floppy disk  
;; COMPUTER: Apple Power Macintosh  
;; OPERATING SYSTEM: Apple Operating System 7.5.5  
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/08/995,659  
;; FILING DATE: 22 DECEMBER 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 60/064,671  
;; FILING DATE: 14 OCTOBER 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 08/813,509  
;; FILING DATE: 07 MARCH 1997  
;;  
;; CLASSIFICATION:  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: USSN 08/772,330  
;; FILING DATE: 23 DECEMBER 1996  
;;  
;; CLASSIFICATION:  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Perkins, Patricia Anne  
;; REGISTRATION NUMBER: 34,693  
;; REFERENCE/DOCKET NUMBER: 2852-A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;;  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 625 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;;  
;; US-08-995-659-15

Query Match 3.2%; Score 9; DB 4; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149  
DB 170 CKPWTNCTL 178

RESULT 23  
US-09-215-649A-15  
Sequence 15 Application US/09215649A  
Patent No. 6271349  
GENERAL INFORMATION:  
APPLICANT: Anderson, Dirk M.  
Galibert, Laurent  
Maraskovsky, Eugene  
TITLE OF INVENTION: Receptor Activator of NF-kappaB  
NUMBER OF SEQUENCES: 19  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Immunex Corporation, Law Department  
STREET: 51 University Street  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98101  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: Apple Power Macintosh

;; OPERATING SYSTEM: Apple Operating System 7.5.5  
;; SOFTWARE: Microsoft Word for Power Macintosh 6.0.1  
;;  
;; CURRENT APPLICATION DATA:  
;; APPLICATION NUMBER: US/09/215,649A  
;; FILING DATE: 17-Dec-1998  
;; CLASSIFICATION: <Unknown>  
;;  
;; PRIOR APPLICATION DATA:  
;; APPLICATION NUMBER: 08/996,139  
;; FILING DATE: <Unknown>  
;; APPLICATION NUMBER: USSN 08/813,509  
;; FILING DATE: 07 MARCH 1997  
;; APPLICATION NUMBER: USSN 08/772,330  
;; FILING DATE: 23 DECEMBER 1996  
;;  
;; ATTORNEY/AGENT INFORMATION:  
;; NAME: Perkins, Patricia Anne  
;; REGISTRATION NUMBER: 34,693  
;; REFERENCE/DOCKET NUMBER: 2851-A  
;; TELECOMMUNICATION INFORMATION:  
;; TELEPHONE: (206)587-0430  
;; TELEFAX: (206)233-0644  
;;  
;; INFORMATION FOR SEQ ID NO: 15:  
;; SEQUENCE CHARACTERISTICS:  
;; LENGTH: 625 amino acids  
;; TYPE: amino acid  
;; TOPOLOGY: linear  
;; MOLECULE TYPE: protein  
;; SEQUENCE DESCRIPTION: SEQ ID NO: 15:  
;;  
;; US-09-215-649A-15

Query Match 3.2%; Score 9; DB 4; Length 625;  
Best Local Similarity 100.0%; Pred. No. 1.3;  
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149  
DB 170 CKPWTNCTL 178

RESULT 24  
US-09-105-390-20  
Sequence 20 Application US/09105390  
Patent No. 6288303  
GENERAL INFORMATION:  
APPLICANT: Rodriguez, Raymond  
TITLE OF INVENTION: Rice Beta-Glucanase Enzymes  
NUMBER OF SEQUENCES: 66  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Denlinger & Associates  
STREET: 350 Cambridge Ave., Suite 250  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94306  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/105,390  
FILING DATE: Filed herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 60/050,675  
FILING DATE: 25-JUN-97  
ATTORNEY/AGENT INFORMATION:  
NAME: Pelithory, Joanne R.  
REGISTRATION NUMBER: P42,995  
REFERENCE/DOCKET NUMBER: 2000-0455.30  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-324-0880



TELEFAX: 650-324-0960  
TELEX:  
; INFORMATION FOR SEQ ID NO: 20:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 30 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; FRAGMENT TYPE: internal  
US-09-105-390-20

Query Match 2.5%; Score 7; DB 4; Length 30;  
Best Local Similarity 100.0%; Pred. No. 6.9;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20  
Db 13 AALLLLG 19

RESULT 25  
US-09-124-671-17  
; Sequence 17, Application US/09124671A  
; Patent No. 6160088  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee  
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
; FILE REFERENCE: 31488  
; CURRENT APPLICATION NUMBER: US/09/124,671A  
; CURRENT FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 17  
; LENGTH: 105  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric mouse TSP3-KDEL  
US-09-124-671-17

Query Match 2.5%; Score 7; DB 4; Length 105;  
Best Local Similarity 100.0%; Pred. No. 22;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20  
Db 9 AALLLLG 15

RESULT 26  
US-09-124-671-19  
; Sequence 19, Application US/09124671A  
; Patent No. 6160088  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee  
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
; FILE REFERENCE: 31488  
; CURRENT APPLICATION NUMBER: US/09/124,671A  
; CURRENT FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 19  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:

; OTHER INFORMATION: chimeric mouse TSP3-KDEL  
US-09-124-671-19

Query Match 2.5%; Score 7; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20  
Db 9 AALLLLG 15

RESULT 27  
US-09-124-671-21  
; Sequence 21, Application US/09124671A  
; Patent No. 6160088  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee  
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
; FILE REFERENCE: 31488  
; CURRENT APPLICATION NUMBER: US/09/124,671A  
; CURRENT FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 21  
; LENGTH: 109  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric Xenopus laevis TSP4-KDEL  
US-09-124-671-21

Query Match 2.5%; Score 7; DB 4; Length 109;  
Best Local Similarity 100.0%; Pred. No. 23;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20  
Db 9 AALLLLG 15

RESULT 28  
US-09-124-671-13  
; Sequence 13, Application US/09124671A  
; Patent No. 6160088  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee  
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
; FILE REFERENCE: 31488  
; CURRENT APPLICATION NUMBER: US/09/124,671A  
; CURRENT FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO 13  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric rat comp  
US-09-124-671-13

Query Match 2.5%; Score 7; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 14 AALLLLG 20

DB 9 AALLLG 15

## RESULT 29

US-09-124-671-15  
; Sequence 15, Application US/09124671A  
; Patent No. 6160088  
; GENERAL INFORMATION:  
; APPLICANT: Rothman, James  
; APPLICANT: Mayhew, Mark  
; APPLICANT: Hoe, Mee  
; TITLE OF INVENTION: KDEL RECEPTOR INHIBITORS  
; FILE REFERENCE: 3148  
; CURRENT APPLICATION NUMBER: US/09/124,671A  
; CURRENT FILING DATE: 1998-07-29  
; NUMBER OF SEQ ID NOS: 42  
; SOFTWARE: FastSeq for Windows Version 3.0  
; SEQ ID NO: 15  
; LENGTH: 115  
; TYPE: PRT  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: chimeric rat COMP-KDEL  
US-09-124-671-15

Query Match 2.5%; Score 7; DB 4; Length 115;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 AALLLG 20  
DB 9 AALLLG 15

RESULT 30  
US-08-478-039-110  
; Sequence 110, Application US/08478039  
; Patent No. 5681722  
; GENERAL INFORMATION:  
; APPLICANT: Newman, Roland A.  
; APPLICANT: Hanna, Nabil  
; APPLICANT: Raab, Ronald W.  
; TITLE OF INVENTION: Recombinant Antibodies for Human Therapy  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
; STREET: 699 Prince St.  
; CITY: Alexandria  
; STATE: VA  
; COUNTRY: USA  
; ZIP: 2213-1404  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC Compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/478,039  
; FILING DATE: 07-JUN-1995  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/379,072  
; FILING DATE: 25-JAN-1995  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/912,292  
; FILING DATE: 10-JUL-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/856,281  
; FILING DATE: 23-MAR-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 07/735,064

; FILING DATE: 25-JUL-1991  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Teskin Esq., Robin L.  
; REGISTRATION NUMBER: 35,030  
; REFERENCE/DOCKET NUMBER: 012712-160  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 703-836-6620  
; TELEFAX: 703-836-2021  
; INFORMATION FOR SEQ ID NO: 110:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 128 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-478-039-110

Query Match 2.5%; Score 7; DB 1; Length 128;  
Best Local Similarity 100.0%; Pred. No. 26;  
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 15 AALLGL 21  
DB 4 AALLGL 10

Search completed: June 18, 2002, 14:28:49  
Job time: 207 sec



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Result No.	Score	Query Match	length	DB	ID	Description
1	277	100.0	217	16	AAR74737	ACT-4 cell surface
2	277	100.0	217	16	AAR79904	ACT-4-h-1 receptor
3	277	100.0	217	22	AAB35329	Human OX40 protein
4	277	100.0	217	22	AAB50522	Human tumour necrosis
5	114	41.2	277	16	AAR76896	Deduced sequence of
6	56	20.2	56	20	AAW94649	TNF-R extracellular
7	42	15.2	58	22	AAB69201	Human TNF-R extrac
8	37	13.4	37	22	AAB84272	Secondary signal
9	37	13.4	37	22	AAB98799	Human secondary s
10	37	13.4	41	22	AAB84292	Amino acid sequen
11	37	13.4	41	22	AAB98777	Human secondary s

12	37	13.4	41	22	AAB98872	Human secondary structure
13	32	11.6	33	22	AAB98872	Human secondary structure
14	12	4.3	205	22	AAB66965	Ox40 protein. UniProt
15	12	4.3	206	16	AAR181	Mouse type-II membrane
16	12	4.3	206	19	AAW48977	Mouse Ox40 extracellular
17	12	4.3	438	16	AAR1882	Plasmodium falciparum
18	12	4.3	438	16	AAW48976	Ox40/FC protein. C
19	9	3.2	201	21	AAV59508	OBM binding protein
20	9	3.2	625	19	AAW83200	Murine osteoclast
21	9	3.2	625	19	AAW69598	Murine NF- $\kappa$ B receptor
22	9	3.2	625	21	AAW68254	Murine NF- $\kappa$ B receptor
23	9	3.2	625	21	AAV59509	OBM binding protein
24	9	3.2	625	21	AAV53649	A mouse receptor for
25	9	3.2	625	22	AAE08739	Murine receptor for
26	9	3.2	625	22	AAE04427	Murine receptor for
27	9	3.2	625	22	AAE01994	Murine RANK (receptor
28	9	3.2	625	21	AAV44302	Mouse osteoclast
29	8	2.9	51	22	ABG01304	Novel human diaphanous
30	8	2.9	51	22	ABG18404	Novel human diaphanous
31	8	2.9	87	22	ABG01184	Novel human diaphanous
32	8	2.9	114	20	AAW87305	A cysteine rich so
33	8	2.9	122	22	ABG01305	Novel human diaphanous
34	8	2.9	132	19	AAW57070	Human secreted protein
35	8	2.9	141	22	ABG18405	Novel human diaphanous
36	8	2.9	190	22	AAW55566	Human reproductive
37	8	2.9	271	22	ABG28519	Novel human diaphanous
38	8	2.9	282	20	AAV32926	Transmembrane domain
39	8	2.9	282	20	AAV13365	Amino acid sequence
40	8	2.9	282	21	AAV97280	Lipid associated protein
41	8	2.9	282	21	AAW24398	Human PRO224 protein
42	8	2.9	282	21	AAV53442	Human PRO224 anti
43	8	2.9	282	21	AAW38847	Human polypeptide
44	8	2.9	282	22	AAU12327	Human PRO224 polypeptide
45	8	2.9	282	22	AAW80233	Human PRO224 protease
46	8	2.9	282	22	AAW53079	Human angiogenesis
47	8	2.9	303	22	AAW40633	Human polypeptide
48	8	2.9	308	22	ABG25452	Novel human diaphanous
49	8	2.9	320	22	ABG01306	Novel human diaphanous
50	8	2.9	335	22	ABG28518	Novel human diaphanous

RESULT	1
AAR74737	
ID	AAR74737 standard; Protein; 277 AA.
XX	
AC	AAR74737;
XX	
DT	21-NOV-1995 (first entry)
XX	
DE	ACT-4 cell surface receptor protein.
XX	
KW	Cell surface receptor; ACT-4; T-Lymphocyte; T
XX	
OS	Homo sapiens.
XX	
FH	key
FT	Peptide
FT	
FT	Cleavage-site
FT	
FT	Cleavage-site
FT	
FT	Modified-site
FT	
FT	Modified-site
FT	
FT	Domain
FT	
PN	WO9512673-A.

XX 11-MAY-1995.  
 PD 03-NOV-1994; 94MO-GB02415.  
 XX 03-NOV-1994; 93US-0147784.  
 PR 03-NOV-1993; 93US-0147784.  
 XX (BECTON ) BECTON DICKINSON CO.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Buck DW, Engleman EG, Godfrey W;  
 PI WPI: 1995-185777/24.  
 DR N-PSDB: AAQ08758.  
 XX Isolated ACT-4 receptor from activated T-cells - also its ligands and  
 PT antibodies, useful for treating diseases of the immune system  
 XX Claim 1; Fig. 5; 82pp; English.  
 PS This sequence encodes the full-length cell surface receptor ACT-4  
 CC isolated from activated CD4+ T-lymphocytes. The sequence may be  
 CC expressed in e.g. COS-7 cells. The encoded protein, its ligands or  
 CC fragments, and antibodies may be used for the treatment of transplant  
 CC rejection, graft-versus-host disease, autoimmune disease, etc.  
 CC  
 XX Sequence 277 AA;

Query Match 100.0%; Score 277; DB 16; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-250;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRGPCAALLLLGLSTVYGLHCYVDITYPSNDRCHCECRPGNGMVSRSRSQ 60  
 DB 1 mcvgarrrlgrgpcaalllllglstvtglhcyvdytysndrchcecrpgngmvsrsrsq 60  
 OY 61 NNYCRPGCGFYNDVYSSKPKCKPCTWCNLRSGSERKQLCTATDITYCRCAAGTQPLDSYK 120  
 DB 61 nnycrpgcgfyndvyskpkckpctwcnlrsgserkqlctatditycrcaagtcpldsyk 120  
 OY 121 PGVDCAPCPGHPSPGDNQCKPMTNCTLAGKHTLQPASNSAICEEDRPPATQPOETQ 180  
 DB 121 pyvdcapcpghpspgdnqackpwtncitlagkhtlqpasnsaicedrppatqpgetq 180  
 OY 181 GPPARPITVQPTAMPRTSGPSTRREVYVGGRAVAAILGLGLVTLGLPLAILLALYLL 240  
 DB 181 gpparpltvqpteamprtsqgstrevyvggravaaillglglvtlglplailallalyll 240  
 OY 241 RRDQRLPPDAHKRPGGSGFRTPIQEODAHSTLAKI 277  
 DB 241 rrdqrlppdahkppgsgsfrtpiqeodahstlaki 277

## RESULT 2

AAR79904  
 ID AAR79904 standard; Protein: 277 AA.

AC AAR79904;

DT 05-MAR-1996 (first entry)  
 XX ACT-4-h-1 receptor sequence.

DE ACT-4; specific binding partner: sbd; B cells; lymphocyte; GVHD;  
 KW graft versus host disease; immune response; transplantation;  
 KW autoimmune disease; inflammation; HIV; human immunodeficiency virus;  
 KW HTLV; human T lymphocyte virus; inflammatory bowel disease;  
 KW screening; identification.

OS Homo sapiens.

XX key 4 Location/Qualifiers

FT Cleavage-site 22..23 /note= "Possible cleavage site."  
 FT Cleavage-site 24..25 /note= "Possible cleavage site."  
 FT Modified-site 136..138 /label= Glycosylation site.  
 FT Modified-site 150..152 /label= Glycosylation site.  
 FT Domain 204..230 /label= Transmembrane domain.  
 XX  
 PN W09521915-A1.  
 XX 17-AUG-1995.  
 PD 06-FEB-1995; 95MO-GB00238.  
 XX 10-FEB-1994; 94US-0195967.  
 PR (GREA/) GREAVES C P.  
 PA (STRD ) UNIV LELAND STANFORD JUNIOR.  
 XX Engleman EG, Godfrey W;  
 PI WPI: 1995-293117/38.  
 DR N-PSDB: AAT04048.  
 XX Ligand, ACT-4-1, to receptor on activated CD4 positive cells  
 PT useful in treatment of various immune diseases and conditions  
 PS Disclosure; Figure 5; 124pp; English.

CC ACT-4-1-h-1 is a specific binding partner (sbp) to the ACT-4  
 CC receptor polypeptide (encoded by this sequence) on the surface of  
 CC activated CD4 positive B cells. The sbp and its fragments are useful  
 CC in pharmaceutical compositions to modify a patient's immune response  
 CC as well as having application in the treatment of transplant  
 CC rejection, graft versus host disease, autoimmune disease, HIV,  
 CC inflammation, infectious agents, HTLV infected cells or HTLV.  
 CC Specifically the sbd can be used to treat inflammatory bowel  
 CC disease. The sbd can also be used for screening for immunomodulatory  
 CC agents able to recognise ACT-4 and for monitoring activated CD4  
 CC positive cells or inhibiting infection of CD4 positive cells.

XX Sequence 277 AA;

Query Match 100.0%; Score 277; DB 16; Length 277;  
 Best Local Similarity 100.0%; Pred. No. 2.7e-250;  
 Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MCVGARRLGRGPCAALLLLGLSTVYGLHCYVDITYPSNDRCHCECRPGNGMVSRSRSQ 60  
 DB 1 mcvgarrrlgrgpcaalllllglstvtglhcyvdytysndrchcecrpgngmvsrsrsq 60  
 OY 61 NNYCRPGCGFYNDVYSSKPKCKPCTWCNLRSGSERKQLCTATDITYCRCAAGTQPLDSYK 120  
 DB 61 nnycrpgcgfyndvyskpkckpctwcnlrsgserkqlctatditycrcaagtcpldsyk 120  
 OY 121 PGVDCAPCPGHPSPGDNQCKPMTNCTLAGKHTLQPASNSAICEEDRPPATQPOETQ 180  
 DB 121 pyvdcapcpghpspgdnqackpwtncitlagkhtlqpasnsaicedrppatqpgetq 180  
 OY 181 GPPARPITVQPTAMPRTSGPSTRREVYVGGRAVAAILGLGLVTLGLPLAILLALYLL 240  
 DB 181 gpparpltvqpteamprtsqgstrevyvggravaaillglglvtlglplailallalyll 240  
 OY 241 RRDQRLPPDAHKRPGGSGFRTPIQEODAHSTLAKI 277  
 DB 241 rrdqrlppdahkppgsgsfrtpiqeodahstlaki 277

RESULT 3

AAB35329  
ID AAB35329 standard; Protein: 277 AA.  
XX  
AC AAB35329;  
XX  
DT 08-MAY-2001 (first entry)  
XX  
DE Human OX40 protein SEQ ID NO: 3.  
XX  
KW Human; tumour necrosis factor receptor; TR13; TR14; infection;  
KW cancer; autoimmune disease; allergy; inflammatory disease;  
KW graft rejection; apoptosis; cardiovascular disease; aneurysm.  
XX  
OS Homo sapiens.  
XX  
PN WO200105834-A1.  
XX  
PD 25-JAN-2001.  
XX  
PE 14-JUL-2000; 2000WO-US19343.  
XX  
PR 16-JUL-1999; 99US-0144087.  
PR 18-AUG-1999; 99US-0149450.  
PR 20-AUG-1999; 99US-0149712.  
PR 10-SEP-1999; 99US-0153089.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Ruben SM, Ni J, Young PE.  
XX  
DR WPI: 2001-112682/12.  
XX  
PT Nucleic acids encoding 2 human tumor necrosis factor receptor  
PT polypeptides (TR13) and (TR14); useful for the prevention, diagnosis  
PT and treatment of, e.g. cancers, acquired immune deficiency syndrome and  
PT hypohidrotic ectodermal dysplasia -  
XX  
PS Disclosure; Page 372-373; 418pp; English.  
XX  
CC The present invention provides the protein and coding sequences of the  
CC human tumour necrosis factor receptors TR13 and TR14. These sequences are  
CC useful in the diagnosis and treatment of many diseases, including cancer,  
CC autoimmune diseases, cardiovascular disorders, allergies,  
CC neurodegenerative diseases, graft rejection, inflammation, aneurysms and  
CC infections.  
XX  
SQ Sequence 277 AA;  
  
Query Match 100.0%; Score 277; DB 22; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.7e-250;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCVGARRLGRPCALLLLGLSTVTVGLHCVGDTYPSNDRCHBCRPGNGVNSRCSRSQ 60  
DB 1 MCVGARRLGRPCALLLLGLSTVTVGLHCVGDTYPSNDRCHBCRPGNGVNSRCSRSQ 60  
QY 61 NTVCRCGPGFYNDVSSKPKCTMCNLRSGSERKOLCTATODPYVCRAGTOPLDSYK 120  
DB 61 ntvcrcpgpgfyndvsskpkctmcnllrsgserkqclctatqdtvcrcrqtqpldsyk 120  
QY 121 PGVDCAPCPGHSFGDNOACKPWTNCTLAGKHTLQPASNSSDAICEDRDPATQPGETQ 180  
DB 121 pgvdcapcpghsfpgdnoackpwtncnctlagkhtlqpasnsdalcdrdpapatqpgetq 180  
QY 181 GPRARPTVQTEAMPRTSOGPSTRPVEVPGGRAVAALLGLGLVGLGPIALLIATLYL 240  
DB 181 gprarptlvqteamprrtsogpstrpvevpggravaaillglglvlgllgpialla1lyl1 240  
QY 241 RRQRLPPDAKPPGSGSFRPTIOEQADASTLAKI 277  
DB 241 rrqrlppdaakppgsgsfrptioeqadastlaki 277

RESULT 4  
AAB50522  
ID AAB50522 standard; Protein: 277 AA.  
XX  
AC AAB50522;  
XX  
DT 15-MAR-2001 (first entry)  
XX  
DE Human tumour necrosis factor receptor OX40 protein SEQ ID NO:12.  
XX  
KW Human; tumour necrosis factor receptor 5; TR1D; TNFR-5; TR5; neutrotic;  
KW TRAIL receptor without intracellular domain; diagnosis; cytostatic;  
KW tumour necrosis factor related apoptosis inducing ligand; vasotropic;  
KW immunosuppressive; neuroprotective; antiviral; antiinflammatory;  
KW anticonvulsant; antiparasitic; cardiant; anti-HIV; antiparkinsonian;  
KW gene therapy; restenosis; graft versus host disease; tumour; cancer;  
KW apoptotic cell death related disease; autoimmune disorder;  
KW cardiovascular disorder; viral infection.  
XX  
OS Homo sapiens.  
XX  
PN WO200071150-A1.  
XX  
PD 30-NOV-2000.  
XX  
PE 18-MAY-2000; 2000WO-US13515.  
XX  
PR 20-MAY-1999; 99US-0135164.  
XX  
PA (HUMA-) HUMAN GENOME SCI INC.  
XX  
PI Wel Y, Ruben SM, Gentz RL, Ni J;  
XX  
DR WPI: 2001-041051/05.  
XX  
PT Nucleic acid encoding a TR1D polypeptide, also referred to as tumor  
PT necrosis factor receptor 5, useful in the diagnosis, treatment or  
PT prevention of cancer, autoimmune disorders and viral infection -  
XX  
PS Disclosure; Fig 2; 285pp; English.  
XX  
CC The present invention describes the human TR1D protein (tumour necrosis  
CC factor (TNF) related apoptosis inducing ligand (TRAIL) receptor without  
CC intracellular domain, also referred to as tumour necrosis factor  
CC receptor 5 (TNFR-5 or TR5)). TR1D has cytostatic, immunosuppressive,  
CC neutrotic, neuroprotective, antiviral, antiinflammatory, anticonvulsant,  
CC antiparasitic, cardiant, anti-HIV, antiparkinsonian and vasotropic  
CC activities, and can be used in gene therapy. The TR1D polynucleotides  
CC are useful for detecting complementary polynucleotides. TR1D proteins and  
CC polynucleotides are useful in the treatment of tumours, resistance to  
CC parasite, bacteria and viruses, restenosis and graft versus host disease.  
CC They are also useful for inducing proliferation of T-cells, endothelial  
CC cells and certain haematopoietic cells, to regulate antiviral responses  
CC and to prevent certain autoimmune diseases after stimulation of TR1D by  
CC an agonist or TRAIL binding facilitator. The antibodies which bind TR1D  
CC polypeptides are useful for treating and/or preventing diseases  
CC associated with increased or decreased apoptotic cell death. The TR1D  
CC polynucleotides, proteins, antibodies, agonists and antagonists are  
CC useful in the diagnosis, treatment or prevention of: (a) cancer;  
CC (b) autoimmune disorders; (c) diseases associated with increased  
CC apoptosis; (d) cardiovascular disorders; and (e) viral infection. The  
CC present sequence represents a tumour necrosis factor receptor used in  
CC comparison with TR1D in the exemplification of the present invention.  
XX  
SQ Sequence 277 AA;  
  
Query Match 100.0%; Score 277; DB 22; Length 277;  
Best Local Similarity 100.0%; Pred. No. 2.7e-250;  
Matches 277; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
QY 1 MCVGARRLGRPCALLLLGLSTVTVGLHCVGDTYPSNDRCHBCRPGNGVNSRCSRSQ 60

```

Db      1  |||
        1  mcvgartrlgpcca1111g1stvtglhcvygdtypsndrcchecrpgnwmvscrsiq 60
Oy      61  NTVCRCPCGPGFYNDVVSRSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQPLDYSK 120
        61  ntvcrcpgpgfyndvvsrskpcpkctwcnlrsgerkqlctacqdlvcrcragtqpldysk 120
Oy      121  PCVDCAPCPGPHFSPGDNAQCKRWNTNCTLAGKHTLQPASNSSDALCEDRDPAPOPTQ 180
        121  pcvdcapcpghfspdnaqckrwnctlagkhtlqpasnsdalcdrdpapoptq 180
Db      181  GPAPARTVQPTFAMPRTSQSGSTRVEVPGRAVAALLGLGVGLPLALLLALLYL 240
        181  gpapartvqptfamprtsqsgstrvevpgravaallglgvglplalllallyl 240
Oy      241  RRDQRLPPDAHKPCGSGSFRTPIOEQADAHSTLAKI 277
        241  rrdqrlppdahkpcgsgsfrtpioeqadahstlaki 277
Db      241  rtdqrlppdahkpcpgsgsfrtptlqeeqadahstlaki 277

RESULT  5
AAR76996
ID      AAR76996 standard; Protein; 277 AA.
XX
AC      AAR76996;
XX
DT      21-DEC-1995 (first entry)
XX
DE      Deduced sequence encoded by human OX-40 cDNA.
XX
KW      Human OX-40; activated T-cells; CD4+ T-cells; antigen;
KW      multiple sclerosis; sarcoidosis; rheumatoid arthritis; uveitis;
KW      T-cell lymphoma.
XX
OS      Homo sapiens.
XX
PN      WO9521251-A.
XX
PD      10-AUG-1995.
XX
PE      06-FEB-1995; 95WO-CB00237.
XX
PR      04-FEB-1994; 94US-0192480.
XX
PA      (WEIN/) WEINBERG A D.
PA      (CANT-) CANTAB PHARM RES LTD.
XX
PI      Vandenberg AA, Weinberg AD;
XX
DR      WPI: 1995-283771/37.
DR      N-PSDB: AA093257.
XX
PT      Nucleic acid encoding an activated T-cell antigen, OX-40 - used to
PT      develop prods. for detection and therapy of conditions mediated by
PT      activated T-cells, eg. multiple sclerosis, rheumatoid arthritis, etc.
XX
PS      Claim 3; Fig 11; 91pp; English.
XX
CC      Antigen OX-40 is specifically expressed on the cell surface of
CC      antigen activated T-cells, especially, for example, CD4+ T-cells. A
CC      human cDNA encoding the human OX-40 homologue was cloned as follows.
CC      Using the experimental autoimmune Encephalomyelitis model in rats
CC      the OX-40 antigen was identified (expressed on the surface of
CC      activated autanigen-specific CD4+ T-cells present at the site of
CC      inflammation but absent on CD4+ T-cells at non-inflammatory sites)
CC      and cDNA encoding the antigen was isolated. PCR primers were
CC      designed and used to clone murine OX-40 cDNA by PCR from RNA
CC      isolated from murine CD4+ T-cells activated with concanavalin A.
CC      The murine OX-40 cDNA was used to probe a cDNA lambda gt11
CC      library from human activated T lymphocytes to obtain human OX-40
CC      cDNA. The published patent application states that the OX-40 cDNA
CC      sequence is also in SO ID no. 1, but this sequence is not present
CC      in the spec. A nucleic acid having the sequence in SO ID no 1 and

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CC      the polypeptide encoded by it are claimed.
XX
SO      Sequence 277 AA:

Query Match 41.2%; Score 114; DB 16; Length 277;
Best Local Similarity 100.0%; Pred. No. 3.8e-98;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      1  MCVGARLRGRCPCALLLLGLSTVTGLHCVGDTYPSNDRCHECRCPGNGVSRCSRSQ 60
        1  mcvgartrlgpcca1111g1stvtglhcvygdtypsndrcchecrpgnwmvscrsiq 60
Db      61  NTVCRCPCGPGFYNDVVSRSKPCPKCTWCNLRSGSERKOLCTATODTVCRCRAGTQ 114
        61  ntvcrcpgpgfyndvvsrskpcpkctwcnlrsgerkqlctatqdlvcrcragtq 114
Db      61  ntvcrcpgpgfyndvvsrskpcpkctwcnlrsgerkqlctatqdlvcrcragtq 114

RESULT  6
AAM94649
ID      AAM94649 standard; peptide; 56 AA.
XX
AC      AAM94649;
XX
DT      29-APR-1999 (first entry)
XX
DE      TNF-R extracellular Cys-rich domain OX40.
XX
KW      Tumour necrosis factor receptor; TNF-R; autoimmune diseases;
KW      inflammation; septic shock; cachexia; graft versus host disease;
KW      skin allergic reaction; Immune complex disease; malaria;
KW      transplantation rejection.
XX
OS      Homo sapiens.
XX
PN      WO9853842-A1.
XX
PD      03-DEC-1998.
XX
PE      29-MAY-1998; 98WO-US10891.
XX
PR      30-MAY-1997; 97US-0866545.
XX
PA      (UYPE-) UNITV PENNSYLVANIA.
XX
PI      Greene MI, Murali R, Takasaki W;
XX
DR      WPI: 1999-080781/07.
XX
PT      New compounds designed from a binding loop of a tumour necrosis
PT      factor receptor - are capable of inhibiting the biological
PT      activities of tumour necrosis factor, e.g., in treating inflammation
PT      or autoimmune diseases
XX
PS      Disclosure; Fig 1; 78pp; English.
XX
CC      The present invention describes peptides and peptide analogues which
CC      correspond in primary sequence to a binding loop of a tumour necrosis
CC      factor receptor (TNF-R) superfamily member. The compounds are especially
CC      designed from a binding loop of TNF-R p55. They are capable of
CC      inhibiting TNF binding to its cellular receptors and may be used to
CC      inhibit the biological activities of TNF. They may be used in treating
CC      TNF-associated conditions such as acute and chronic inflammatory
CC      responses, septic shock, cachexia, autoimmunity, graft-versus-host
CC      disease, skin allergic reactions, immune complex disease,
CC      transplantation rejection and malaria. Administration is, e.g. oral,
CC      transmucosal, intramuscular, pulmonary, subcutaneous, intravenous or
CC      intranasal. Parenteral dosage is 0.1-5 mg/kg/day. The present
CC      sequence represents an extracellular Cys-rich domain of TNF-R from the
CC      present invention.
XX
SO      Sequence 56 AA:

```



Query Match 20.2%; Score 56; DB 20; Length 56;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-44;  
 Matches 56; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 CRPCGPGFYNDVSSKPKCTWNCNLRSGSERKOLCTAOTDTCVCRAGTGPLDSY 119  
 Db 1 crpcpgpfyndvsskpkctwncnlrsgserkqlctatqdtvcragtgpldsy 56

## RESULT 7

AAB69201  
 ID AAB69201 standard; protein; 58 AA.

AC AAB69201;

DE 30-APR-2001 (first entry)

XX Human TNF-R extracellular Cys-rich domain OX40 SEQ ID NO:10.

XX Tumour necrosis factor receptor; TNF-R; inhibition; osteoclast;

KW osteoclastogenesis; bone loss; bone resorption; osteopathic; cytostatic;

KW antineumatic; antiarthritic; antiinflammatory; immunomodulatory;

KW tumour necrosis factor-related activation-induced cytokine; TRANCE;

KW receptor activator of NF-kappaB ligand; RANK; osteoporosis;

KW periodontal disease; metastatic bone disease; rheumatoid arthritis;

KW T cell proliferation; CD40 receptor system.

XX Homo sapiens.

XX WO200108699-A1.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20510.

XX 28-JUL-1999; 99US-0146090.

XX (UYPE-) UNIV PENNSYLVANIA.

XX (AOKI/) AOKI K.

XX (HORN/) HORNE W C.

XX (BARO/) BARON R.

XX Aoki K, Horne WC, Baron R, Greene MI, Murali R;

XX WPT: 2001-182866/18.

XX Use of peptides and peptide analogs which are TRANCE/RANK inhibitors,

XX for inhibiting osteoclastogenesis and bone resorption

XX Disclosure: Fig 1; 81pp: English.

XX The present invention describes a method for inhibiting

XX osteoclastogenesis and bone resorption. Osteoclastogenesis and bone

XX resorption inhibiting peptide analogues from the present invention have

XX osteopathic, cytostatic, antineumatic, antiarthritic, antiinflammatory

XX and immunomodulatory activities, and are tumour necrosis factor (TNF)-

XX NF-kappaB ligand (RANK) inhibitors. The method is useful for treating

XX diseases characterised by bone loss such as osteoporosis, Paget's

XX disease, metastatic bone disease, rheumatoid arthritis or periodontal

XX disease, and modulating dendritic cell maturation, T cell proliferation,

XX and/or CD40 receptor systems. The present sequence represents an

XX extracellular Cys-rich domain of a tumour necrosis factor receptor

XX (TNF-R) superfamily member, which is used in the exemplification of

XX the present invention.

SO Sequence 58 AA;

Query Match 15.2%; Score 42; DB 22; Length 58;  
 Best Local Similarity 100.0%; Pred. No. 1.7e-31;

Matches 42; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 64 CRPCGPGFYNDVSSKPKCTWNCNLRSGSERKOLCTAOTDTCVCRAGTGPLDSY 105  
 Db 1 crpcpgpfyndvsskpkctwncnlrsgserkqlctatqdt 42

## RESULT 8

AAB84272  
 ID AAB84272 standard; peptide; 37 AA.

AC AAB84272;

DE 22-AUG-2001 (first entry)

XX Secondary signalling sequence used to make cytoplasmic signalling motif.

KW Stimulatory primary signalling motif; immune cell; signal transduction;

KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;

KW eczema; congenital disease; cystic fibrosis; sickle cell anemia;

KW dermatological disease; psoriasis; neurological disease;

KW multiple sclerosis; transplant-related disease; metabolic disease;

KW organ transplant rejection; graft versus host disease;

KW idiopathic disease; diabetes; cancer.

OS Synthetic.

XX WO200132709-A2.

XX 10-MAY-2001.

XX 01-NOV-2000; 2000WO-GB04183.

XX 01-NOV-1999; 99GB-0025848.

XX (CELL-) CELLTech CHIROSCIENCE LTD.

XX Finney HM, Lawson ADG;

XX WPT: 2001-389718/41.

XX Novel cytoplasmic signalling protein and chimeric receptor protein,

XX useful for treating HIV infection, asthma, eczema, psoriasis, multiple

XX sclerosis, contain non-natural stimulatory primary signalling motif -

XX Claim 15; Page 29; 45pp: English.

XX The present sequence represents a secondary signalling sequence, which

XX is linked to a non-natural stimulatory primary signalling motif to

XX produce a cytoplasmic signalling motif. The primary motif is efficient

XX at mediating immune cell signal transduction, particularly when

XX incorporated in an intracellular signalling domain of a chimeric

XX receptor. The primary signalling motif can be combined in any way so

XX as to achieve the desired level of activation (or inhibition) of a

XX number of secondary messenger cascades. The signalling motifs are useful

XX in therapy and in the manufacture of medicament for treating or

XX preventing disease in humans or animals. They are useful for treating

XX human patients suffering from infectious diseases e.g. human

XX immunodeficiency virus (HIV) infections, inflammatory/autoimmune diseases

XX such as asthma and eczema, congenital diseases e.g. cystic fibrosis,

XX sickle cell anemia, dermatological diseases e.g. psoriasis, neurological

XX diseases e.g. multiple sclerosis, transplant-related disease e.g. organ

XX transplant rejection, graft versus host disease, metabolic/idiopathic

XX disease e.g. diabetes, and cancer.

SO Sequence 37 AA;

Query Match 13.4%; Score 37; DB 22; Length 37;  
 Best Local Similarity 100.0%; Pred. No. 5.3e-27;  
 Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 241 RRDORLPPDAHKPPGGGSRFTPIQEOBDAHSTLAKI 277

Db 1 rrdqrlppdahkppggsftrtpeqeadahstlakt 37

## RESULT 9

AAB98799 ID AAB98799 standard; Peptide: 37 AA.

AC AAB98799;

DT 08-AUG-2001 (first entry)

DE Human secondary signalling motif SB34a.

KW Human; anti-HIV; antiinflammatory; antiaesthetic; dermatological;  
KW antischleim; antipruritic; neuroprotective; immunosuppressive;  
KW antidiabetic; cytostatic; HIV infection; inflammation;  
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;  
KW neurological disease; organ transplant rejection; diabetes; cancer;  
KW graft-versus-host disease; adaptor receptor protein; CD28; CD134; CD154;  
KW primary signalling motif; secondary signalling motif.

OS Homo sapiens.

XX WO200132866-A2.

PN 10-MAY-2001.

PD 01-NOV-2000; 2000WO-GB04189.

PF 01-NOV-1999; 99GB-0025854.

PR (CELL-) CELLTech CHIROSCIENCE LTD.

PA Flinney HM, Lawson ADG;

PI WPI: 2001-328790/34.

DR Novel polynucleotide encoding adaptor receptor protein useful for

PT treating human immunodeficiency virus (HIV) infection, asthma, cystic

PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and

PT cancer -

PS Claim 26; Page 35; 52pp; English.

XX The invention relates to a novel nucleic acid encoding an adaptor  
CC receptor protein comprising an extracellular ligand-binding domain, a  
CC transmembrane domain and an intracellular signalling domain. The  
CC intracellular signalling domain comprises the cytoplasmic portion of at  
CC least one adaptor protein, and the extracellular ligand-binding domain  
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.  
CC The adaptor receptor protein and the nucleic acid encoding it are useful  
CC in therapy. They are useful in the manufacture of a medicament for the  
CC treatment or prevention of disease in humans and animals. They are useful  
CC in the treatment of infectious diseases (e.g. HIV infection),  
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),  
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),  
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g. )  
CC multiple sclerosis), organ transplant rejection, graft-versus-host  
CC disease and metabolic/idiopathic diseases such as diabetes and cancer.  
CC The present sequence is a secondary signalling motif used in the  
CC invention. Secondary signalling motifs impart secondary or co-stimulatory  
CC signalling capacity to a molecule in T cells. They may be used as  
CC components of the adaptor receptor protein of the invention. Motifs were  
CC isolated from CD28, CD134 and CD154.

XX Sequence 37 AA:

Query Match 13.4%; Score 37; DB 22; Length 37;  
Best Local Similarity 100.0%; Pred. No. 5.3e-27;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDQLRPPDAHkPPGGSFRTPIQEQADAHSTLAKI 277  
Db 1 rrdqrlppdahkppggsftrtpeqeadahstlakt 37

## RESULT 10

AAB84292 ID AAB84292 standard; peptide: 41 AA.

AC AAB84292;

DT 22-AUG-2001 (first entry)

DE Amino acid sequence of a secondary signalling sequence.

KW Stimulatory primary signalling motif; immune cell; signal transduction;  
KW chimeric receptor; inflammatory disease; autoimmune disease; asthma;  
KW eczema; congenital disease; cystic fibrosis; sickle cell anaemia;  
KW dermatological disease; psoriasis; neurological disease;  
KW multiple sclerosis; transplant-related disease; metabolic disease;  
KW organ transplant rejection; graft versus host disease;  
KW idiopathic disease; diabetes; cancer.

OS Synthetic.

XX WO200132709-A2.

PN 10-MAY-2001.

PD 01-NOV-2000; 2000WO-GB04183.

PF 01-NOV-1999; 99GB-0025848.

PR (CELL-) CELLTech CHIROSCIENCE LTD.

PA Flinney HM, Lawson ADG;

PI WPI: 2001-389718/41.

DR Novel cytoplasmic signalling protein and chimeric receptor protein,

PT useful for treating HIV infection, asthma, eczema, psoriasis, multiple

PT sclerosis, contain non-natural stimulatory primary signalling motif -

PS Example 2; Fig 4; 45pp; English.

XX The present sequence represents a secondary signalling sequence, which  
CC may be linked to a non-natural stimulatory primary signalling motif  
CC The primary motif is efficient at mediating immune cell signal  
CC transduction, particularly when incorporated in an intracellular  
CC signalling domain of a chimeric receptor. The primary signalling motif  
CC can be combined in any way so as to achieve the desired level of  
CC activation (or inhibition) of a number of secondary messenger cascades.  
CC The signalling motifs are useful in therapy and in the manufacture of  
CC medicament for treating or preventing disease in humans or animals. They  
CC are are useful for treating human patients suffering from infectious  
CC diseases e.g. human immunodeficiency virus (HIV) infections,  
CC inflammatory/autoimmune diseases such as asthma and eczema, congenital  
CC diseases e.g. cystic fibrosis, sickle cell anaemia, dermatological  
CC diseases e.g. psoriasis, neurological diseases e.g. multiple sclerosis,  
CC transplant-related disease e.g. organ transplant rejection, graft versus  
CC host disease, metabolic/idiopathic disease e.g. diabetes, and cancer.

XX Sequence 41 AA:

Query Match 13.4%; Score 37; DB 22; Length 41;  
Best Local Similarity 100.0%; Pred. No. 5.8e-27;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 241 RRDQLRPPDAHkPPGGSFRTPIQEQADAHSTLAKI 277  
Db 3 rrdqrlppdahkppggsftrtpeqeadahstlakt 39

RESULT 11  
ID AAB98777 standard; Peptide: 41 AA.  
AC AAB98777;  
DT 07-AUG-2001 (first entry)  
DE Human secondary signalling motif sequence block SB34.  
KW Human: primary signalling motif; sequence block; SB; immunosuppressive;  
KW secondary signalling sequence; antimicrobial; anti-inflammatory;  
KW dermatological; neuroprotective; cytostatic; anti-HIV; antiasthmatic;  
KW antiskilling; antipsoriatic; antidiabetic; gene therapy; diabetes;  
KW immune cell signal transduction; infection; inflammation; cancer;  
KW autoimmune disease; congenital disease; psoriasis; neurological disease;  
KW organ transplant rejection.  
OS Homo sapiens.  
PN WO200132867-A1.  
PD 10-MAY-2001.  
PE 01-NOV-2000; 2000WO-GB04193.  
PR 01-NOV-1999; 99GB-0025853.  
PA (CELL-) CELLTECH CHIROSCEINCE LTD.  
PI Flinney HM, Lawson ADG;  
DR WPI; 2001-328791/34.  
XX New nucleic acids encoding polypeptides with expanded primary signalling  
PT motifs, for use in gene therapy, particularly for treating or  
PT preventing infections, inflammations or autoimmune diseases in humans  
PS -  
XX Example 2; Fig 4; 43pp; English.  
XX The invention relates to novel primary signalling motifs containing  
CC a consensus amino acid sequence. These motifs are extremely  
CC efficient at mediating immune cell signal transduction, particularly  
CC when incorporated into an intracellular signalling domain of a chimeric  
CC receptor. Nucleic acids that encode, and polypeptides that contain,  
CC these primary signalling motifs are useful in medicine and research.  
CC They are useful in therapy, or in the manufacture of a medicament for  
CC treating or preventing disease in humans or in animals. These diseases  
CC include infections (e.g. HIV (human immunodeficiency virus) infection),  
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital  
CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological  
CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple  
CC sclerosis), organ transplant rejection or graft-versus-host disease, or  
CC metabolic/diopathic diseases (e.g. diabetes or cancer). The  
CC present sequence is one of a large number of primary and secondary  
CC signalling motifs used in the invention. Primary signalling motifs are  
CC sequences that transduce either a stimulatory or an inhibitory signal,  
CC which regulates primary activation of the T cell receptor (TCR) complex.  
CC Secondary motifs impart secondary or co-stimulatory signalling capacity  
CC to a molecule in T cells. GS linkers have been incorporated at each  
CC end of the present sequence to facilitate cloning.  
XX  
SQ Sequence 41 AA;  
Query Match 13.4%; Score 37; DB 22; Length 41;  
Best Local Similarity 100.0%; Pred. No. 5.8e-27;  
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
OY 241 RRDRRLPPDAHKPPGGSFRPIQEGADAHSTLAKI 277  
|||||

DB 3 rrdqrlppdahkppggsfrpigeqadahlaki 39  
RESULT 12  
ID AAB98822 standard; Peptide: 41 AA.  
AC AAB98822;  
DT 08-AUG-2001 (first entry)  
DE Human secondary signalling motif sequence block SB34.  
KW Human: anti-HIV; antiinflammatory; antiasthmatic; dermatological;  
KW antiskilling; antipsoriatic; neuroprotective; immunosuppressive;  
KW antidiabetic; cytostatic; HIV infection; inflammation;  
KW autoimmune disease; cystic fibrosis; sickle cell anaemia; psoriasis;  
KW neurological disease; organ transplant rejection; diabetes; cancer;  
KW graft-versus-host disease; adaptor receptor protein; sequence block;  
KW SB; primary signalling motif; secondary signalling motif.  
OS Homo sapiens.  
PN WO200132866-A2.  
PD 10-MAY-2001.  
PE 01-NOV-2000; 2000WO-GB04189.  
PR 01-NOV-1999; 99GB-0025854.  
PA (CELL-) CELLTECH CHIROSCEINCE LTD.  
PI Flinney HM, Lawson ADG;  
DR WPI; 2001-328790/34.  
XX Novel polynucleotide encoding adaptor receptor protein useful for  
PT treating human immunodeficiency virus (HIV) infection, asthma, cystic  
PT fibrosis, multiple sclerosis, organ transplant rejection, diabetes and  
PT cancer -  
XX  
XX Example 3; Fig 4; 52pp; English.  
XX The invention relates to a novel nucleic acid encoding an adaptor  
CC receptor protein comprising an extracellular signalling domain, a  
CC transmembrane domain and an intracellular signalling domain. The  
CC intracellular signalling domain comprises the cytoplasmic portion of at  
CC least one adaptor protein, and the extracellular ligand-binding domain  
CC is not CD8 or a major histocompatibility complex (MHC) class I protein.  
CC The adaptor receptor protein and the nucleic acid encoding it are useful  
CC in therapy. They are useful in the manufacture of a medicament for the  
CC treatment or prevention of disease in humans and animals. They are useful  
CC in the treatment of infectious diseases (e.g. HIV infection),  
CC inflammatory and autoimmune diseases (e.g. asthma and eczema),  
CC congenital diseases (e.g. cystic fibrosis and sickle cell anaemia),  
CC dermatological diseases (e.g. psoriasis), neurological diseases (e.g.)  
CC multiple sclerosis), organ transplant rejection, graft-versus-host  
CC disease and metabolic/diopathic diseases such as diabetes and cancer.  
CC The present sequence is one of a number of sequence blocks (SBs) of  
CC primary and secondary signalling motifs. Primary signalling motifs  
CC transduce either a stimulatory or an inhibitory signal, which regulates  
CC primary activation of the T cell receptor (TCR) complex. Secondary  
CC signalling motifs impart secondary or co-stimulatory signalling capacity  
CC to a molecule in T cells. Primary and secondary signalling motifs may be  
CC used as components of the adaptor receptor protein of the  
CC invention. The sequence contains a GS linker at the N-terminus to  
CC facilitate cloning.  
XX  
SQ Sequence 41 AA;  
Query Match 13.4%; Score 37; DB 22; Length 41;  
|||||

```
Best Local Similarity 100.0%; Pred. No. 5.8e-27;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Oy      241 RRQRRLPPDAHPPGGSFRTPIQEEADAHSTLAKI 2777
          |||||
Db      3  rrdqrlppdahkppgsgsftrpiqeeqadastlaki 39

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RESULT 13  
AAB98752

ID	standard; Peptide; 32 AA.
XY	

AC AAB98752;

DT 07-AUG-2001 (first entry)

Human secondary signaling motif SB34a

KM Human, primary signalling motif; CD28; CD134; CD154; sequence block; SB  
KM immunosuppressive; secondary signalling sequence; antimicrobial; cancer  
KM antiinflammatory; dermatological; neuroprotective; cytostatic; anti-HIV  
KM antidiabetic; antiscaling; antiparasitic; antidiabetic; gene therapy;  
KM diabetes; immune cell signal transduction; infection; inflammation;  
KM autoimmune disease; congenital disease; psoriasis; neurological disease;  
KM organ transplant rejection.

OS Homo sapiens.

PN WO200132867-A1.

PD 10-MAY-2001  
yy

PF 01-NOV-2000; 2000WO-GB04193.  
VY

PR	01-NOV-1999;	99GB-0025853.
YY		

PA (CELL-) CELLTECH CHIROSCEINCE LTD.  
XY

PI Flney HM, Lawson ADG,  
YY

DR WP1; 2001-328791/34.  
XX

**P1** New nucleic acids encoding polypeptides with expanded primary signaling motifs for use in gene therapy, particularly for treating or

PM - preventing infections, inflammations or autoimmune diseases in humans

XX  
PS  
C1a1m 16: Page 28: English

CC The invention relates to novel primary signalling motifs containing  
CC a consensus amino acid sequence. These motifs are extremely  
CC efficient at mediating immune cell signal transduction, particularly  
CC when incorporated into an intracellular signalling domain of a chimeric  
CC receptor. Nucleic acids that encode, and polypeptides that contain,  
CC these primary signalling motifs are useful in medicine and research.  
CC They are useful in therapy, or in the manufacture of a medicament for  
CC treating or preventing disease in humans or in animals. These diseases  
CC include infections (e.g. HIV (human immunodeficiency virus) infection),  
CC inflammatory or autoimmune diseases (e.g. asthma or eczema), congenital  
CC diseases (e.g. cystic fibrosis or sickle cell anaemia), dermatological  
CC diseases (e.g. psoriasis), neurological diseases (e.g. multiple  
CC sclerosis), organ transplant rejection or graft-versus-host disease, or  
CC metabolic/diopathic diseases (e.g. diabetes or cancer). The  
CC present sequence is a secondary signalling sequence used in the  
CC invention. Secondary signalling sequences impart secondary or  
CC co-stimulatory signalling capacity to a molecule in T cells.  
CC Secondary signalling sequences were isolated from human CD28, CD134  
CC and CD134.

**SQ Sequence 32 AA;**

Query Match: 11.68; Score 32; DB 22; Length 32;

Best Local Similarity	100.0%	Pred. No. 2.2e-22;
Matches 32; Conservative	0;	Mismatches 0; Indels 0; Gaps 0

```
Qy      241  RRDRLLPPDAHKPPGGGSFRTPIQEEQADAHs  272
         |||||
Db      1  rrdgrlppdankppggsfrrlpqeeqadahs  32
```

RESULT 14  
AAB66985

ID	AAB66985 standard; Protein; 205 AA
1	1
2	2
3	3
4	4
5	5
6	6
7	7
8	8
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11	11
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98	98
99	99
100	100

AC AAB66985;

DT 19-APR-2001 (first entry)

Ox40 protein.

KM Bone loss; osteoporogenesis; OPG; rheumatoid arthritis; hyperalgesia;  
KM multiple sclerosis; osteoporosis; osteomyelitis; asthma; inflammation;  
KM systemic lupus erythematosus; graft-versus-host disease; septic shock;  
KM acute pancreatitis; Alzheimer's disease; anorexia; atherosclerosis; pain  
KM coronary condition; myocardial infarction; cancer; diabetes; psoriasis;  
KM endometriosis; fever; glomerulonephritis; inflammatory bowel disease;  
KM ischaemia; Parkinson's disease.

OS Unidentified

PN WO200103719-A2

PD 18-JAN-2001

PF 07-JUL-2000; 2000WO-US186667

PR	09-JUL-1999;	99US-0350670
PR	09-DEC-1999;	99US-0457647

XX (MCE-) AUGEN TUC

XX  
XX

XX  
 FEB. 2001-103031/11

XX  
XX  
E

PT multiple sclerosis and asthma, comprises administering an

Interleukin and tumor necrosis factor

XX The present invention relates to a method for treating conditions leading  
CC to bone loss. The method comprises administering a purified and isolated  
CC osteoprotegerin (OPG) protein (AA6757836-AA6757838 and AA666974-AA666976)  
CC in conjunction with other substances such as tumour necrosis factor- $\alpha$ -  
CC (TNF- $\alpha$ ) inhibitors, interleukin (IL)-6, -8 and -18 inhibitors, ICE  
CC modulators, fibroblast growth factor (FGF)-1-10 modulators and/or platelet  
CC activating factor (PAF) antagonists. The method is useful for treating  
CC conditions leading to bone loss such as rheumatoid arthritis, multiple  
CC sclerosis, osteoporosis, osteomyelitis and asthma. The method is also  
CC useful for treating inflammation, systemic lupus erythematosus (SLE) and  
CC graft-versus-host disease (GVHD). Other diseases that can be treated  
CC include acute pancreatitis, Alzheimer's disease, anorexia,  
CC atherosclerosis, coronary conditions (e.g. myocardial infarction),  
CC cancer, diabetes, endometriosis, fever, glomerulonephritis, hyperalgesia,  
CC inflammatory bowel disease, ischaemia, pain, Parkinson's disease,  
CC psoriasis and septic shock. The present sequence was used in a sequence  
CC homology comparison.  
CX

Best Local Similarity 100.08; Pred. No. 0.0048;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149  
 |||||  
 Db 135 nqackpwtncctl 146

RESULT 15  
 AAR81881  
 ID AAR81881 standard; Protein: 206 AA.

AC AAR81881;  
 DT 08-JUL-1996 (first entry)  
 DE Mouse type-II membrane polypeptide OX40 extracellular domain.  
 KW OX40; OX40-L; cytokine; cell surface molecule;  
 KM membrane glycoprotein.  
 XX  
 OS Mus musculus.  
 PN US5457035-A.  
 XX  
 PD 10-OCT-1995.  
 XX  
 PF 23-JUL-1993; 93US-0097827.  
 XX  
 PR 23-JUL-1993; 93US-0097827.  
 XX  
 PA (IMMV ) IMMUNEX CORP.  
 XX  
 PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
 DR WPI; 1995-357992/46.  
 DR N-PSDB; AAT00826.  
 XX  
 PT New isolated DNA encoding the OX40 ligand polypeptide - also vectors  
 PT and host cells, used to produce recombinant ligand used in e.g.  
 PT prim. T cell culture, to modulate immune response etc.  
 XX  
 PS Example 1; Column 33-34; 26pp; English.  
 XX  
 CC This sequence encodes the extracellular domain of OX40, a membrane  
 CC glycoprotein present on the CD4 positive subset of activated T  
 CC cells.  
 CC  
 SQ Sequence 206 AA;

Query Match 4.3%; Score 12; DB 16; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 0.0048;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149  
 |||||  
 Db 136 nqackpwtncctl 147

RESULT 16  
 AAW48977  
 ID AAW48977 standard; Protein: 206 AA.

AC AAW48977;  
 DT 25-SEP-1998 (first entry)  
 DE Mouse OX40 extracellular domain.  
 KW OX40; cytokine; T cell antigen; TH-2 immune response; OX40-L;  
 KM OX40/Fc.  
 XX  
 OS Mus sp.

XX US5783665-A.  
 PN  
 XX 21-JUL-1998.  
 PD  
 XX  
 PF 22-JUN-1995; 95US-0494574.  
 XX  
 PR 23-JUL-1993; 93US-0097827.  
 PR 22-JUN-1995; 95US-0494574.  
 XX  
 PA (IMMV ) IMMUNEX CORP.

PI Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
 DR WPI; 1998-427099/36.  
 DR N-PSDB; AAV32640.

PT Purified polypeptide OX-40 ligands - for co-stimulation of T-cell  
 PT production and binding assays for OX-40 and homologues  
 XX  
 PS Example 1; Col 33-34; 26pp; English.

XX The present sequence represents the mouse OX40 extracellular domain  
 CC The extracellular domain of OX40 is its ligand binding domain. The  
 CC CDNA (AAV32640) encoding OX40 extracellular domain was used in the  
 CC construction of the chimeric OX40/Fc cDNA (AAV32640). The invention  
 CC claims for a murine OX40-L cytokine (AAW48975) that binds to the OX40  
 CC murine T cell antigen. The OX40-L protein is claimed to be useful  
 CC for co-stimulation of T-cell production and in binding assays for  
 CC detecting OX40 or its homologues. The OX40-L protein is also claimed  
 CC to generate a TH-2 immune response.  
 XX

SQ Sequence 206 AA;

Query Match 4.3%; Score 12; DB 19; Length 206;  
 Best Local Similarity 100.0%; Pred. No. 0.0048;  
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 138 NOACKPWTNCTL 149  
 |||||  
 Db 136 nqackpwtncctl 147

RESULT 17  
 AAR81882  
 ID AAR81882 standard; Protein: 438 AA.

AC AAR81882;  
 DT 30-MAR-1996 (first entry)  
 DE Plasmid pDC406/OX40/Fc\* encoding an OX40/Fc mutein protein.  
 DE  
 XX OX40; OX40-L; cytokine; cell surface molecule; plasmid;  
 KW pDC406/OX40/Fc\*; membrane glycoprotein.  
 KM  
 XX Synthetic.

OS  
 XX US5457035-A.  
 PN  
 XX 10-OCT-1995.  
 PD  
 XX 23-JUL-1993; 93US-0097827.  
 PF  
 XX 23-JUL-1993; 93US-0097827.  
 PR  
 XX 23-JUL-1993; 93US-0097827.  
 PR  
 XX (IMMV ) IMMUNEX CORP.

PA Baum PR, Fanslow WC, Gayle RB, Goodwin RG;  
 PI  
 XX WPI; 1995-357992/46.  
 DR N-PSDB; AAT00829.



Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 141 CKPWTNCTL 149  
 |||||  
 Db 170 ckpwtnctl 178

RESULT 20  
 AAM83200  
 ID AAM83200 standard; Protein: 625 AA.

AC AAM83200;  
 DT 11-FEB-1999 (first entry)

DE Murine osteoclast differentiation and activation receptor.

KW Osteoprotegerin binding protein; OPG binding protein; arthritis;  
 KW osteoporosis; osteoclast maturation; bone disease; metastasis; ODA;  
 KW hypercalcaemia; osteoclast differentiation and activation receptor;  
 KW Paget's disease.

OS Mus sp.

PN WO9846751-A1.

PD 22-OCT-1998.

PF 15-APR-1998; 98WO-US07584.

PR 30-MAR-1998; 98US-0052521.

PR 16-APR-1997; 97US-0842842.

PR 23-JUN-1997; 97US-0880855.

PA (AMGE-) AMGEN INC.

PI Boyle WJ;

DR WPI: 1998-594578/50.

PT Nucleic acid encoding osteoprotegerin binding protein - useful for,  
 PT e.g. treating bone diseases by modulating osteoclast differentiation  
 PT and for diagnosis

PS Example 12; Fig 10; 47pp; English.

CC The present sequence represents murine osteoclast differentiation  
 CC and activation receptor (ODAR). The present invention describes  
 CC osteoprotegerin (OPG) binding protein. Host cells transfected with  
 CC vectors containing nucleic acid molecules encoding OPG binding protein  
 CC are used to produce recombinant OPG binding protein. OPG binding protein  
 CC is used in binding assays to determine osteoprotegerin (OPG) in biological  
 CC samples; to screen for specific binding agents (particularly agonists  
 CC and antagonists), including intracellular proteins; to raise Ab (useful  
 CC in immunoassays for detection of OPG binding proteins) and to identify  
 CC compounds that modulate binding of OPG binding protein to ODAR. The  
 CC nucleic acid molecule encoding OPG binding protein can be used to detect  
 CC OPG binding protein-encoding sequences, e.g. screening for related  
 CC sequences, also to produce transgenic animal models, while complementary  
 CC sequences are used for antisense regulation of OPG binding protein  
 CC expression. Modulators of OPG binding protein, particularly soluble  
 CC forms of OPG binding protein or Ab, are used to treat or prevent bone  
 CC diseases, e.g. osteoporosis, bone loss caused by arthritis or  
 CC metastases, hypercalcaemia, Paget's disease, periodontal disease,  
 CC osteoporosis, loosening of prostheses, optionally in combination with  
 CC agents that promote bone growth.

SQ Sequence 625 AA;

Query Match 3.2%; Score 9; DB 19; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 141 CKPWTNCTL 149  
 |||||  
 Db 170 ckpwtnctl 178

RESULT 21  
 AAM69958  
 ID AAM69958 standard; Protein: 625 AA.

AC AAM69958;

DT 08-OCT-1998 (first entry)

DE Murine NF-kB receptor activator mURANK.

KW RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;  
 KW immune response; inflammatory response; toxic shock; sepsis;  
 KW RANKL; RANK ligand; tumour necrosis factor; TNF; murine.

OS Mus sp.

PN WO9828426-A2.

PD 02-JUL-1998.

PF 22-DEC-1997; 97WO-US23775.

PR 14-OCT-1997; 97US-0064671.

PR 23-DEC-1996; 96US-0059978.

PR 07-MAR-1997; 97US-0813509.

PA (IMMV) IMMUNEX CORP.

PI Anderson DM, Gallibert LJ, Maraskovsky E;

DR WPI: 1998-377657/32.

DR N-PSDB; AAV41379.

PT New isolated ligand for receptor activator of NF-kappa B - used to  
 PT develop products for augmenting an immune response for inhibiting an  
 PT inflammatory response and for protection of cells

PS Example 14; Pages 62-64; 80pp; English.

CC This represents the murine mURANK (receptor activator of necrosis  
 CC factor-kappa B (NF-kB)) polypeptide which is a homolog of the human RANK.  
 CC RANK is a member of the tumour necrosis factor (TNF) family. A soluble  
 CC RANK may be used for inhibiting activation of NF-kB, by contacting a cell  
 CC expressing membrane-associated RANK with a soluble RANK which binds to  
 CC RANK ligand (RANKL). RANKL polypeptides can activate RANK and can be  
 CC used to induce maturation of dendritic cells and enhance their  
 CC allo-stimulatory capacity, thereby augmenting an immune response. The  
 CC soluble RANK polypeptide composition may also be used for regulating an  
 CC immune or inflammatory response. Inhibition of NF-kB by RANK antagonists  
 CC may be useful in ameliorating negative effects of an inflammatory  
 CC response that result from triggering of RANK, e.g. in treating toxic  
 CC shock or sepsis, graft-versus-host reactions, or acute inflammatory  
 CC reactions. They can also be used in adjunct therapy for disease  
 CC characterised by neoplastic cells that express RANK. RANKL polypeptides  
 CC can also be used to identify inhibitors of RANK and thus inhibitors of  
 CC an inflammatory response, and also for protecting RANK-expressing cells  
 CC from the negative effects of chemotherapy or the presence of high levels  
 CC of TNF-alpha. The products can also be used for detection and drug  
 CC screening.

SQ Sequence 625 AA;

Query Match 3.2%; Score 9; DB 19; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149  
 ID |||||  
 DB 170 ckpwtnctl 178

## RESULT 22

AAM68294  
 ID AAM68294 standard; Protein; 625 AA.

XX AAM68294;

DT 08-OCT-1998 (first entry)

XX Murine NF-kB receptor activator murANK.

XX RANK; necrosis factor-kappa B; NF-kB; receptor activator; human;

KM Immune response; inflammatory response; toxic shock; sepsis;

XX RANKL; RANK ligand; tumour necrosis factor; TNF; murine.

XX Mus sp.

XX WO9828424-A2.

XX 02-JUL-1998.

XX 22-DEC-1997; 97WO-US23866.

XX 14-OCT-1997; 97US-0064671.

XX 23-DEC-1996; 96US-0059978.

XX 07-MAR-1997; 97US-0813509.

XX (IMV) IMMUNEX CORP.

XX Anderson DM, Gallibert LJ, Maraskovsky E;

XX WPI: 1998-377655/32.

XX N-PSDB: AAV41373.

XX New isolated receptor activator of necrosis factor-kappa B - useful

XX for, e.g. developing products for regulating an immune or

XX inflammatory response, treating toxic shock or sepsis

XX Claim 27; Pages 62-64; 80pp; English.

XX This represents the murine murANK (receptor activator of necrosis

XX factor-kappaB (NF-kB) polypeptide which is a homolog of the human RANK.

XX RANK is a member of the tumour necrosis factor (TNF) family. Host cells

XX transformed or transfected with an expression vector comprising the RANK

XX encoding nucleic acid can be used to produce recombinant RANK protein.

XX The soluble RANK may be used for inhibiting activation of NF-kB, by

XX contacting a cell expressing membrane-associated RANK with a soluble

XX RANK which binds to RANK ligand (RANKL). The soluble RANK polypeptide

XX composition may also be used for regulating an immune or inflammatory

XX response. Inhibition of NF-kB by RANK antagonists may be useful in

XX ameliorating negative effects of an inflammatory response that result

XX from triggering of RANK, e.g. in treating toxic shock or sepsis, graft-

XX versus-host reactions, or acute inflammatory reactions. They can also be

XX used in adjunct therapy for disease characterised by neoplastic cells

XX that express RANK. The products can also be used for detection and drug

XX screening.

XX Sequence 625 AA:

Query Match 3.2%; Score 9; DB 19; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149  
 ID |||||  
 DB 170 ckpwtnctl 178

## RESULT 23

AAV59509  
 ID AAV59509 standard; Protein; 625 AA.

XX AAV59509;

XX 31-MAR-2000 (first entry)

XX OBM binding protein sequence.

XX OBM-BP; OBM binding protein; osteoclast formation promoting factor;

XX bone metabolic disease; osteoporosis; therapy.

XX Mus sp.

XX JP1332581-A.

XX 07-DEC-1999.

XX 20-OCT-1998; 98JP-0316973.

XX 24-MAR-1998; 98JP-0076232.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX WPI: 2000-091362/08.

XX N-PSDB: AAZ49023.

XX A new protein, a DNA and its application

XX Claim 10; Page 15-16; 18pp; Japanese.

XX This sequence is the osteoclast formation promoting factor (OBM)

XX binding protein (OBM-BP) of the invention. The protein is useful as a

XX preventive and/or treating agent for bone metabolic diseases such as

XX osteoporosis. Substances which inhibit the binding of OBM to OBM-BP can

XX be used as biochemical reagents.

XX Sequence 625 AA:

Query Match 3.2%; Score 9; DB 21; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 141 CKPWTNCTL 149  
 ID |||||  
 DB 170 ckpwtnctl 178

## RESULT 24

AAV53649  
 ID AAV53649 standard; Protein; 625 AA.

XX AAV53649;

XX 22-FEB-2000 (first entry)

XX A mouse receptor activator of NF-kappaB designated RANK.

XX Mouse; receptor; RANK; Receptor activator of NF-kappaB;

XX osteoclast activity; immune response; inflammatory response;

XX excess bone resorption; osteoclast generation; bone loss; osteoporosis;

XX Paget's disease; bone cancer; cancer; hypercalcemia; osteoclastogenesis;

XX metastasizing cancer; osteoclast differentiation; signal transduction.

XX Mus sp.

XX WO9958674-A2.

XX 18-NOV-1999.



XX 13-MAY-1999; 99MO-US10588.  
 XX 14-MAY-1998; 98US-0085487.  
 PR 03-DEC-1998; 98US-0110836.  
 XX (1MMV ) IMMUNEX CORP.  
 PA Anderson DM, Galibert LJ;  
 PI WPI: 2000-053099/04.  
 DR N-PSDB: AAZ36258.  
 XX  
 PT Novel cytokine receptors for regulating osteoclast activity to  
 ameliorate excess bone loss effects of osteoporosis, Paget's disease,  
 PT bone cancers etc  
 XX  
 PS Disclosure; Page 25-27; 28pp; English.  
 XX  
 CC The present sequence represents a soluble murine receptor designated RANK  
 CC (Receptor activator of NF-kappaB). The protein is used to regulate  
 CC osteoclast activity. The RANK protein or its fragments are useful for  
 CC regulating an immune or inflammatory response, especially to decrease  
 CC excess bone resorption, and for inhibiting osteoclast activity,  
 CC regulating osteoclast generation and inhibiting osteoclast generation  
 CC in individuals afflicted with excess bone resorption. Especially, the  
 CC RANK protein is used to treat individuals at risk for excess bone loss,  
 CC osteoporosis, Paget's disease, bone cancer and cancers associated with  
 CC hypercalcemia. The RANK protein ameliorates the effects of excess bone  
 CC loss, by binding to its ligand and inhibiting binding of other cells  
 CC expressing RANK. It thus decreases osteoclastogenesis when administered  
 CC into metastasizing cancers such as breast cancer, multiple myeloma,  
 CC melanomas, lung cancer, prostate, hematologic, head and neck, and renal  
 CC which metastasize to bone and induce bone breakdown by locally disrupting  
 CC normal bone remodeling, by disrupting the osteoclast differentiation  
 CC pathway. This results in the reduction in the number of osteoclasts,  
 CC lesser bone resorption and relief from the negative effects of  
 CC hypercalcemia. The RANK protein also ameliorates systemic effects by  
 CC interfering with I/I signal transduction that leads to the  
 CC differentiation of osteoclast precursors into osteoclasts.  
 XX  
 SQ Sequence 625 AA;  
 Query Match 3.2%; Score 9; DB 21; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 141 CKPWTNCTL 149  
 Db 170 ckpwncntl 178  
 RESULT 25  
 AAE08739  
 ID AAE08739 standard; Protein: 625 AA.  
 XX  
 AC AAE08739;  
 XX  
 DT 15-NOV-2001 (first entry)  
 XX  
 DE Murine receptor activator of NF kappaB (RANK) protein.  
 XX  
 KW Murine: receptor activator of nuclear factor kappaB; RANK; NF;  
 KW tumour necrosis factor; TNF; TNF receptor associated factor; TRAF;  
 KW immune response; inflammatory response; graft-versus-host reaction;  
 KW toxic shock; sepsis; acute inflammatory reaction; bone resorption;  
 KW anti-apoptotic signal; therapy; immunosuppressant; anti-inflammatory.  
 OS Mus sp.  
 XX  
 FH Key Location/Qualifiers  
 FT Peptide 1..30

FT /label= signal\_peptide  
 FT Protein 31..625  
 FT /label= Mature\_RANK\_protein  
 XX  
 PN US6271349-B1.  
 XX  
 PD 07-AUG-2001.  
 XX  
 PF 17-DEC-1998; 98US-0215649.  
 XX  
 PR 23-DEC-1996; 96US-0059978.  
 PR 07-MAR-1997; 97US-0077181.  
 PR 14-OCT-1997; 97US-0064671.  
 PR 23-DEC-1996; 96US-0772330.  
 PR 07-MAR-1997; 97US-0813509.  
 PR 22-DEC-1997; 97US-0996139.  
 XX  
 PA (1MMV ) IMMUNEX CORP.  
 XX  
 PI Dougall WC, Galibert LJ;  
 XX  
 DR WPI: 2001-520313/57.  
 DR N-PSDB: AAD15312.  
 XX  
 PT New receptor activator of NF-kappaB (RANK) polypeptides, useful for  
 PT regulating immune response, in screening for RANK inhibitors, or as an  
 PT adjunct therapy for disease characterized by neoplastic cells that  
 PT express RANK  
 XX  
 XX Example 14; Column 77-80; 47pp; English.  
 XX  
 CC The patent discloses novel receptor activator of nuclear factor (NF)-  
 CC kappaB (RANK) proteins and their corresponding DNAs. RANK is a member  
 CC of the tumour necrosis factor (TNF) receptor superfamily and associates  
 CC with TNF receptor associated factor (TRAF) 2 and 3 which are important  
 CC in the regulation of immune and inflammatory response. The receptors  
 CC are useful for regulating immune response and in screening for inhibitors  
 CC of these receptors. The cytoplasmic domain of RANK is used in developing  
 CC assays for inhibitors of signal transduction, e.g. for screening the  
 CC molecules that inhibit interaction of RANK with TRAF1, TRAF2, TRAF3,  
 CC TRAF5 and particularly TRAF6. NF-kappaB inhibition by RANK antagonists  
 CC are useful in ameliorating the negative effects of an inflammatory  
 CC response that result from triggering of RANK, e.g. in treating toxic  
 CC shock or sepsis, graft-versus-host reactions, acute inflammatory  
 CC reactions and the effects of bone resorption. RANK acts as an anti-  
 CC apoptotic signal and rescue the cells that express RANK from apoptosis.  
 CC Soluble forms of the receptor are used in vivo or in vitro based  
 CC screening tests for agonists or antagonists of RANK activity, as  
 CC antagonists of RANK-mediated NF-kappa B activation, or to inhibit  
 CC transduction of a signal via RANK. RANK compositions are used in the  
 CC development of both agonistic and antagonistic antibodies, or as an  
 CC adjunct therapy for disease characterized by neoplastic cells that  
 CC express RANK. Compounds that interfere with RANK/TRAF6 interactions  
 CC are useful for modulating the formation of osteoclasts from osteoclast  
 CC precursors and for modulating osteoclast function and activities. They  
 CC are used as inhibitors of diseases associated with excess bone resorption  
 CC and as immunosuppressants or anti-inflammatory agents. The RANK DNAs are  
 CC useful for the expression of recombinant proteins, as probes for analysis  
 CC of the presence or distribution of RANK transcripts, while the proteins  
 CC are useful in preparing kits for the detection of soluble RANK, or  
 CC monitor RANK-related activity. The present sequence is RANK protein  
 CC from murine.  
 XX  
 SQ Sequence 625 AA;  
 Query Match 3.2%; Score 9; DB 22; Length 625;  
 Best Local Similarity 100.0%; Pred. No. 7.8;  
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 141 CKPWTNCTL 149  
 Db 170 ckpwncntl 178

```

RESULT 26
AAE04427
ID AAE04427 standard; Protein; 625 AA.
XX
XX AAE04427;
AC
XX
XX
XX 04-SEP-2001 (first entry)
DT
XX
XX Murine receptor activator of NF- $\kappa$ B (murANK) protein.
DE
XX
XX Murine; receptor activator of NF- $\kappa$ B; RANK; tumour necrosis factor;
KM CD40; TNF receptor-associated factor; TRAF; ligand; immune response; TNF;
KM chromosome 18q22.1; RANKL; chromosome 13q14; transmembrane protein.
XX
XX Mus sp.
OS
XX
XX Key Location/Qualifiers
FH Region 197..214
FT /note="Spacer region"
XX
XX US6242213-B1.
PN
XX
XX 05-JUN-2001.
PD
XX
XX 22-DEC-1997; 97US-0995659.
PF
XX
XX 23-DEC-1996; 96US-0059978.
PR 07-MAR-1997; 97US-0077181.
PR 14-OCT-1997; 97US-0064671.
XX
XX (IMNV ) IMMUNEX CORP.
PA
XX
XX Anderson DM;
PI
XX
XX WPI: 2001-407216/43.
DR N-PSDB: AAD08716.
XX
XX New DNA molecules, useful for producing ligands (which are useful for
PT regulating immune response and in screening for inhibitors of NF- $\kappa$ B
PT receptor activator) of the receptor activator of NF- $\kappa$ B (RANK) -
PT
XX
XX Example 14; Column 71-74; 43pp; English.
PS
XX
XX The present invention relates to receptor activator of NF- $\kappa$ B (RANK)
CC DNA. RANK is mapped to chromosome 18q22.1 and its ligand (RANKL) to
CC chromosome 13q14. RANK and RANKL are type 1 and type 2 transmembrane-
CC proteins respectively. RANK is a member of the tumour necrosis factor
CC (TNF) superfamily and it closely resembles CD40 in the extracellular
CC region. RANK associates with TNF receptor-associated factor (TRAF) 2
CC and TRAF3. The DNA molecules are useful for producing ligands of RANK.
CC The ligands are useful for regulating immune response and in screening
CC for inhibitors of RANK. The present sequence is murine RANK
CC (murANK) protein.
CC
XX
XX Sequence 625 AA:
SQ

```

```

Query Match 3.2%; Score 9; DB 22; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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```

OY 141 CRPWTNCTL 149
DB 170 ckpwtnctnl 178

```

```

RESULT 27
AAE01994
ID AAE01994 standard; Protein; 625 AA.
XX
XX AAE01994;
AC

```

```

XX
XX 31-JUL-2001 (first entry)
DT
XX
XX Murine RANK (receptor activator of NF- $\kappa$ B) protein.
DE
XX
XX Mouse; receptor activator of NF- $\kappa$ B; RANK; nuclear factor- $\kappa$ B;
KM NF- $\kappa$ B; tumour necrosis factor; TNF; type I transmembrane protein;
KM TNF receptor-associated factor; TRAF; RANK ligand; osteopetrotic;
KM inflammatory reaction; bone resorption; gene therapy; immunomodulator;
KM immune system dysfunction; familial expansile osteolysis; FEO;
KM early onset Paget's disease of bone; EP; cytostatic.
XX
XX Mus musculus.
OS
XX
XX Key Location/Qualifiers
FH Region 197..214
FT /label= Spacer_Region
XX
XX WO200136637-A1.
PN
XX
XX 25-MAY-2001.
PD
XX
XX 14-NOV-2000; 2000WO-US31459.
PF
XX
XX 17-NOV-1999; 99US-0442029.
PR
XX
XX (IMNV ) IMMUNEX CORP.
PA
XX
XX Anderson DM, Hughes AE;
PI
XX
XX WPI: 2001-329222/34.
DR N-PSDB: AAD05905.
XX
XX New DNA encoding a receptor activator of NF- $\kappa$ B polypeptide for the
PT treatment of Paget's disease and Familial Expansile Osteolysis (FEO) -
PT
XX
XX Example 14; Page 80-82; 96pp; English.
PS
XX
XX The present invention relates to a novel receptor, referred to as RANK
CC (receptor activator of NF (nuclear factor)- $\kappa$ B), a member of TNF
CC (tumour necrosis factor) receptor superfamily. RANK is a type I
CC transmembrane protein that interacts with TNF receptor-associated
CC factors (TRAFs). Trisegling of RANK by overexpression or co-expression
CC of RANK and membrane bound RANK ligand (RANKL) results in upregulation
CC that is most extensively utilised in cells of the immune system.
CC inhibition of NF- $\kappa$ B by RANK antagonists is useful in ameliorating
CC negative effects of inflammatory reactions, and the effects of excess
CC bone resorption. The RANK DNAs, proteins and their analogues are useful
CC for the preparation of pharmaceutical compositions, for infecting target
CC cells for use in gene therapy applications in diagnosing diseases
CC associated with RANK, and as targets for use in screening assays. They
CC may be used in the treatment or diagnosis of immune system dysfunction.
CC The present invention also encompasses gene therapy methods to correct
CC gene-activating mutations, associated with e.g. familial expansile
CC osteolysis (FEO) and early onset Paget's disease of bone (EP). The
CC present amino acid sequence is murine RANK (murANK) protein. This
CC sequence which is a type I transmembrane protein contains a predicted 30
CC amino acid signal sequence, a 184 amino acid extracellular domain, a 21
CC amino acid transmembrane domain and a 390 amino acid cytoplasmic tail.
CC
XX
XX Sequence 625 AA:
SQ

```

```

Query Match 3.2%; Score 9; DB 22; Length 625;
Best Local Similarity 100.0%; Pred. No. 7.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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OY 141 CRPWTNCTL 149
DB 170 ckpwtnctnl 178

```

```

RESULT 28
AAV44302
ID AAV44302 standard; Protein; 2126 AA.
XX
AC AAV44302;
XX
DT 29-FEB-2000 (first entry)
XX
DE Mouse acrosome reaction protein-PKDREJ.
XX
KM Acrosome reaction protein; P3; sperm protein; polycystin-1; sureJ;
KM Polycystic Kidney Disease and Receptor for Egg Jelly protein; PKDREJ;
KM zona pellucida; fertility; contraceptive; gene therapy; mouse.
XX
OS Mus musculus.
XX
PN WO9964457-A1.
XX
PD 16-DEC-1999.
XX
PF 10-JUN-1999; 99MO-GH01839.
XX
PR 10-JUN-1998; 98GB-0012534.
XX
PA (MED1-) MEDICAL RES COUNCIL.
XX
PI Harris PC, Hugues JR, Ward CJ;
XX
DR WPI; 2000-097518/08.
XX
DR N-PSDB; AAZ29336.
XX
PT New functional mammalian acrosome reaction protein, useful for
PT fertility treatment -
XX
PS Claim 1; Fig 2; 40pp; English.
XX
CC The present sequence is a functional mouse acrosome reaction protein,
CC PKDREJ or P3. PKDREJ is a sperm protein involved in binding the sperm
CC to the egg and/or triggering the acrosome reaction. It exhibits
CC homology to human polycystin-1 and sureJ. It can be used to
CC identify antibodies or proteins that block the acrosome reaction and
CC compounds that trigger acrosome reaction in the absence of zona
CC pellucida. Molecules that enhance the efficacy of the acrosome reaction
CC protein can be used to increase fertility and those blocking its
CC action can be used as contraceptives. DNA encoding PKDREJ can be used in
CC gene therapy and also as primer or probe for identifying sequences that
CC encode mutant forms of acrosome reaction protein.
XX
SQ Sequence 2126 AA;

Query Match 3.2%; Score 9; DB 21; Length 2126;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 ALLLGLGL 23
Db 6 allllglgl 14

RESULT 29
ABG01304
ID ABG01304 standard; Protein; 51 AA.
XX
AC ABG01304;
XX
DT 13-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #1295.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX

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OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSEQ-) HYSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
DR N-PSDB; AAS65491.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 31663; 103pp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on human
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 51 AA;

Query Match 2.9%; Score 8; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 LLLGLGL 23
Db 22 llllglgl 29

RESULT 30
ABG18404
ID ABG18404 standard; Protein; 51 AA.
XX
AC ABG18404;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #18395.
XX
KM Human; chromosome mapping; gene mapping; gene therapy; forensic;
KM food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.

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XX WO200175067-A2.
XX
XX 11-OCT-2001.
XX
XX 30-MAR-2001; 2001WO-US08631.
XX
XX 31-MAR-2000; 2000US-0540217.
XX
XX 23-AUG-2000; 2000US-0649167.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Drmanac RT, Liu C, Tang YT;
XX
XX WPI; 2001-639362/73.
XX
XX N-PSDB; AAS82591.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity -
XX
XX Claim 20; SEQ ID No 48763; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pcl_sequences.
XX
XX Sequence 51 AA;
XX
SQ

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Query Match          2.9%: Score 8; DB 22; Length 51;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 16 LLLGLGL 23
   |||||
DB 22 LLLGLGL 29

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Search completed: June 18, 2002, 14:29:26  
 Job time: 219 sec